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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compagen Ltd.
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(without alignments)
544,454 Million cell updates/sec
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Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARTES

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ALIGNMENTS

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61 VILSVERHKULMAENDEVSSLALDVAARYFYPVILLALEVESHADGEEHSKASAEVA 120	1 MSENGSFANDOBAGGMAVERGMSGAGSARRSHIPERRWARALSAVLIVIIAVIAVANII 60	Query Match 59.9%; Score 1142; DB 13; Length 354; Best Local Similarity 60.0%; Pred. No. 4.8e-84; Matches 21t, Schwervative (x. Mismatches 75; Indels 1), Gaps 3	SECTENCE 354 AA; 39931 MW; FORENZERERARRID CROS4;	PROSITE: PS00237; G_PROTEIN_RECERTOP: UNKNOWN_1.	CERTAIN SECTION MELATINICS.	R PEINTS: PROCEST, MELATONINE.	INTERPRO, IEE002279,	INTERPRO: IPROO276;	INTERPROPERENCE OF THE PROPERTY OF THE PROPERT	EMBL; U67881; AAB48391.1; -:	EMBL; U67882; AAB48392.1;		Morgan J.P., Guardiola B., Delagrange P., Marullo S., Strosberg A.D.;	Jookers R. Petit L., Lacroix I., de Coppet P. Rarrett P.,	TISSUE=SKIN;	SEQUENCE FROM N.A.		NCBI_TaxID=8355;		Amphibia: Batrachia, Amura, Mesobatrachia, Pipoidea, Pipidae:	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	Xenopus laevis (African clawed frog).	MEL-10(B) MELATONIN RECEPTOR.	01-00T-2000 (TrEMBLrel. 15, Last annotation update)	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)	01-MAY-1997 (TrEMBLrel. 03, Created)	P87496;	P87496 PRELIMINARY: PRT; 354 AA.	XULT 1

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RESULT
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Matches 214
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Enkaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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INTERPRO: IPR000275: -.
INTERPRO: IPR000279: -.
PPAM: PF00001: 7tm_1: 1.
PPAM: PF00001: 7tm_1: 1.
PPAM: PF00000: MELATONING.
PRINTS: PR01150: MELATONING.
PRINTS: PR01150: MELATONING.
PROSITE: PF001247: 6_PP-151N_R9:PF076: UNKNOWN_1.
SEQUENCE: 354 AA: 39881 MW; BCF78D208FUC97A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67879; AAB48390.1; -. EMBL; U67879; AAB48389.1; -.
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Morgan J.E., Gudidioia B., Deiagrange F., Marullo S., Stros
Sibmitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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233 KUIQTOLRNELIMEVVEVLEAVCWAPLNEIGLAVAINEENVAEKIEEWLEVLSYIMAYEN 292
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                                    241 CLKPSDLRSFLTMFVVFVIFAICWAPLNCIGLAVAINPQEMAPQIPEGLFVTSYLLAYFN 300
                                                                                                                   181 LEYDDRIYSCTETQTASTQYTAAVVVIHELLBIAVVSECYLRIWVLVLQAFFKAKPESRL 240
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                                                                            LQYDPRIFSCTFAQTVSSSYTITVVVVHFIVPLSVVTFCYLRIWVLVIQVKHRVRQDFKQ 232
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                                                                                                                                                                                                                                           VILSVLRNKKLQNAGNLFVVSLSIADLVVAVYPYPVILIAIFQNGWTLGNIHCQISGFLM 112
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59.4%; Fr
59.4%; Fr
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9: Mismatches 77:
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INTERPRO: IPP002078;
PEAM; PF00001; 7tm_1; 1.

PEINTS: PF00237; GP0PF10PSN
PRINTS: PR01012; MELATONINR.
PRINTS: PR01149; MELATONINAR
PRINTS: PR01149; MELATONINAR
PRINTS: PR01149; MELATONINAR
PROSITE: PR01149; MELATONINAR
PROS
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation updat
MELATONIN RECEPTOR MFL1A.
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi:
Actinopterygii; Neopterygii; Teleostei: Euteleostei;
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                                                                                                                                                                                                                                                                                                        DASKGSHAEGLQSPAPPIIGVQHQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVSFCYLRIWVLVLQAREKAKPESFLCLKPSDLRSELTMEVVEVVIFAICWAPLNCIGLAV 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Mismatches
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SEQUENCE
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Arrain Res Mol Brain Res (0.0-0(1408))

EMBL: APO61158 - AAAG67241 1: -
INTERPRO: IPP000275 - .

INTERPRO: IPP000276 - .
                                       046508:
01-JUN-1998 (TrEMBLrel.
01-HUN-1998 (TrEMBLrel
01-HUN-2000 (TrEMBLrel
              MEL 1A MELATONIN RECEPTOR Ovis aries (Sheep)
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INTERPRO: IPR002278: -
PEAM: PE00001; Ttm_l; 1.
PPINTS: PR00237 . SPCERHODOPSN
PRINTS: PR00857: MELATONINE.
PRINTS: PR00857: MELATONINE.
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01-MAY-1000 (TrEMBLrel 10, Last sequence update)
01-CCT-2000 (TrEMBLrel 15, Last annotation update)
MELATONIN RECEPTOR MELIA (FRAGMENT).
Mesocricetus auratus (Golden hamster)
Eukaryota, Metazea, Chordata, Craniata, Vertebrata,
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae,
 Fukaryota: Metazca: Chordata,
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TISSUE-SUPRACHIASMATIC NUCLEI;
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                                                                                                                                                                                                                    KRIULALWNPPHCIQDAS 337
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                                                                                                                                                                                                                                                                                                                                          YTAAVVVIHELLPIAVVSECYLBIWVLVLQAPBKAKHESELGLKESELPSELIMEVVIVI 156
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Pred. No. 1.3e-78;
1, Mismatches 62;
Crabiata
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Poirel V.J., Pevet P., Gauer F.;
"Rat MT2 melatonin receptor partial cDNA.";
Sibmitted (APF-1999) to the EMM(AMERBACK,COBT delabases
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Barrett P., Gonway S., Jockers P., Strosberg A.D.,

Guardiola-Lemaitre B., Delagrange P., Morgan P.J.;

"Cloning and functional analysis of a polymorphic."

Mel la melatonin receptor.";
                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata: Craniata: Vortebrata: Futelpostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Muridae: Rat
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
MT2 MELATONIN RECEPTOR MEL-1B (FRAGMENT).
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PRINTS: PROCEST; MELATONINAR.
PROSTITE; PROCEST, GENERAL RECEPTOR THENOWN_1.
SECULENCE 366 AA: 40449 MW, HATIMGEFFF; 378FF
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INTERPRO; IPROOD276; -
INTERPRO; IPROC2278; -
PFAM; PF00001; 7tm_1;
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Bovidae: Caprinae: Ovis
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સક 14:
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Pred Wo. 1
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Best Local (
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Best Local Similarity 84.5%;
Matches 147, Couservative
                                                                                                                                                                                            Matches 103:
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncorhynchus mykiss (Painbow trout) (Salmo gairdneri).
Eukaryota: Mctazoa: Chordata: Craniata: Vertebrata: Euteleostemi;
Actinopterygii: Neopterygii: Teleostei: Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mazurais D., Brierley I., Anglade I., Drew J., Kandali C., brownichel D., Kab C., Williams L.M.:
"Central melatonin received to the rainbow trout: comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TREMBLIE). 13, Greated)
01-MAY-2000 (TREMBLIE). 13, Last sequence update)
01-OCT-2000 (TREMBLIE). 15, Last annotation update)
MELATONIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cabt 33
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FFAM: PROUZL7: Thm.! 1.
FFINTS: PROUZL7: GPCRHEDDOPSN.
FFINTS: PROUB57: MELATONINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99306591; PubMed-10379923; Marurais D., Brierley I., Anglade I., Drew J., Randall C., Bricmage N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Comp. Neurol. 409:313-324(1999).
EMBL: AF178929; AAL51850.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         distribution of ligand binding and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF141863; AAF65601.1; -.
                                                                                                                                                                                                                                                                                                                                   Keceptor
                                                                                                                                                                                                                                                                                                                                                 PRINTS: PR01149; MELATONIN1AR
                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 YOYLOHSMAYHRIYRRWHTPLHIGLIWLLTVVALLPNFFVGSLEYDPRIYSCTFIQTAST 198
                  260 FAICWAPLNCIGLAVAINPQEMAPQIPEGLEVTSYLLAYENS 301
                                                                                  200 YTAAVVVIHELLPIAVVSECYLPIWVLVLQARPKAKPESPLCLKPSDLRSELTMEVVEVI 259
                                                                                                                                                       140 CYICHSMAYHRIYRRWRTPLHICLIWLLTVVALLPNFFVGSLEYDPRIYSCTFIQTASTQ 199
                                                                                                                                                                                                              Local cimilarity
                                                                                                                      1 CYICHNLKYDKLESNONTVCYVILVWSLTVLAIVPNWEMESLQVDPRVYSCTEAQSVSSS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | OYTAAVVV.HEELLPIAVVSECYLRIWVLVLQARRKAKPESRLCLKPSDLRSELTMEVVFV 258
                                                 YTITVVVIHEEVPIAVVTECYLRIWILVIQVPPKVKSEVKSPLKPSOMPNEITMEVVEVL 120
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174 1
174 AA;
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                                                                                                                                                                                                                                                                                152 AA:
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                162
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                                                                                                                                                                                                                                                                                18895 MW; 18180915180BAB7B CPC64;
                                                                                                                                                                                            32: Mismatches
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                                                                                                                                                                                                          Score 591; DB 13;
Prod No 3 46-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 780; DB 11;
Pred. No. 2.6e-55;
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                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                            27:
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                                                                                                                                                                                                                              Length 162;
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Db 121 FAICWAPENFIGLAVAIDPETVAPFIPEWEFVVSYFMAYFNS 162
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Best Local Similarity
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Whater D F. Lin C , Reppert S M .
Submitted (MAY-1446) to the EMBL/GenBank/DDBJ databases
EMBL; U57554; AAB17865.1; -.
INTERPPO: 1PR000025; -.
                                                                                                                                                                                                      P70329
P70329;
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SEQUENCE
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                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Redentia;
                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-00T-2000 (TrEMBLrel 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTEPPRO: IPPOCO276: -
PFAM: PFOCOOL: 7tm_1: 1.
PFINTS: PPOC237: GPCPPHODOPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magninis D., Prierley I., Anglade I., Drew J., Par
Michel D., Kah O., Williams L.M.;
"Central metatonin receptors in the rainbow trook
                                                                                                 NCRI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPINTS; PPOOS57; GECREHODOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99306591; PubMed=10379923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                        SEQUENCE FROM N.A.
                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                     MEL-18 MELATONIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF178538; AAD54384.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPROGO025;
                                                                                                                                                                                                                                                                                                                                                                                                              140 CYICHSMAYHRIYRRWHTPLHICLIWHHTVVALLENEFVGSLEYDRRIYSCTEIQTASTQ 199
                                                                                                                                                                                                                                                                                  121 FAVCWAPLNFIGLAVAINPR-LGVNIPEWLFTASYFMAYFNS 161
                                                                                                                                                                                                                                                                                                 260 FAICWAPLNCIGLAVAINPÓEMAPÓIPEGLFVTSYLLAYFNS 301
                                                                                                                                                                                                                                                                                                                                    61 YTITVVVVHEILEISIVTYCYLPIWILVLQVPPPVKPDTPPKIKPHDFHIELTMFVVFVL 120
                                                                                                                                                                                                                                                                                                                                                                                    1 CYICHNLKYDKLESNONTVCYVILVWSLTVLAIVPNWFMESLOYDPRVYSCTFAOSVSSL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
.iši AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.3%;
                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      34, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 556.5;
                                                                                                                 Sciurognathi: Muridae:
                                                                                                                                                                                                                     PRT;
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                                                                                                                  Murinae: Mus
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                             Elavsky N.E., Ernst C.W., Messer L.A., Rothschild M.E., "Identification of Sequence Tagged Sites in the Asian Elephant (Elephas maximus) and the African Elephant (Loxodonta africana)." Submitted (MAR-1947) to the EMBL/Naphank/DDM/ databases EMBL: U95047; AAD00768.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elephas maximus (Indian elephant).
Sukaryota: Metaros, Chordata, Craniata, Vertebrata, Eu-
Mammalia: Eutheria: Proboscidea: Elephantidae; Elephas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TIEMBLIE). 10. Created)
01-MAY-1999 (TIEMBLIE). 10. Last sequence update)
01-UNI-2000 (TIEMBLIE). 14. Last annotation update)
MELATONIN RECEPTOR 1A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   097777
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NON_TER 121 121
SEQUENCE 121 AA: 14055 MW: A2x7505E02450B10 GR054:
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PRINTS: PR00857; MELATONINR.
PRINTS: PR01149; MELATONIN1AH
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                                                                                                                                                                                                                                                                                                                          INTERPRO: IPRO02278: -
PEAM; PF00001; 7tm_1;
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                       Receptor.
                                                                                                                                                                                                                                                                                                                                                     INTERPRO: IPROCO276: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N A
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                                                                                                      NEIGLVVSLDPASMVPP 138
                        NCIGLAVAINPQEMAPO 284
                                         HEIVEMTIVIETYKLEIMVIVLLAPMEVERTEKKEKIKELKELENEVIMEVVEVLEALTUMAEL 121
                                                                                                                                 YHRIYRRWHIPIHICIIWLLIVVALLENEEVOSLEYEPRIYSCIFIQIASIQYIAAVVVI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYTAAVVAIHELLEMAVVSEGYLEIWYLYLQAFEKAKAFEKLELFESDLESELTMEAVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OYTAAVVVIHELLPIAVVSFCYLRIWVLVIQARPKAKPESRLCLKPSDLRSELTMEVVEV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCCICHSTTYHRVCSHWYTPIYISLVWLLTLVALVPNFFVGSLEYDPRIYSCTFIQTAST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCYTCHSMAYHPIYPRWHTPLHICLIWLLTVVALLPNFEVGSLEYDPRIYSCIFIQIASI 198
                                                                              HELLPIAVVSECYLBIWVIVLQABPKAKPESSICIKPSDLBSELTMEVVEVIDSICWARI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97;
                                                                                                                                                                            Similarity
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138
138 AA
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPFLIMINARY:
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                                                                                                                                                                          22.7%;
55.5%;
                                                                                                                                                                                                                               16116 MW-
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80.2%;
                                                                                                                                                              29; Mismatches
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Pred. No. 3.5e-35;
                                                                                                                                                                         Score 433.
Pred No 1
                                                                                                                                                                                                                              BN724084564×hA20 08064;
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اد
                                                                                                                                                                            DB 6,
1 4e-27;
                                                                                                                                                              32;
                                                                                                                                                                                       Length 138
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Best Local Similarity
Matches 94, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       larhammar D;
DNA Cell Biol: 0:0-0(1997).
EMBL; AF030245; AAB94016.1; --
ZFIN: ZDB-GENE-980526-208; npyryb.
INTERPRO; IPR000511; --
PFAM: PF00001; 7tm_1; 1.
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057463;
                                                                   Q9UIYI:
Q1-MAY-2000 (TrEMBLrol 13, Croated)
Q1-MAY-2000 (TrEMBLrol 13, Last sequence update)
Q1-UN-2000 (TrEMBLrol 14, Last dimodation update)
DJ753D10.1 (SOMATOSTATIN RECEPTOR 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS: PRO0237; GPCRRHODOPSN.
PRINTS: PRO0237; GPCRHODOPSN.
PRINTE: FS00237; GPCRHODOPSN.
THE FS00237; GPCRHODOPSN.
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Cypriniformes: Cyprinidae: Bashorinae. Danio.
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Brachydanio rerio (Zebrafish) (Zebra danio)
Pukarvota: Metazoa; Chordata; Craniata; Ver
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01-JUN-1998 (TrEMBLIFE) 06, Last sequence up
01-JUN-2000 (TrEMBLIFE) 14, Last annotation
NEUPOPEPTIDE Y /PEPTIDE YY PECEPTOR YB.
      Eukaryota: Metazoa: Choroata: Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide.
SEQUENCE 375 AA; 42116 MW; 48009551131A14D1 CRC64;
                                              Homo sapiens (Human)
                                                               SSTR4
                                                                                                                                                                TAINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPYRYB
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindell
                                                                                                                                                                                                                                                                                                                                                                                191
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                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                              303 LNAIVYGLLNQNFRREYKRIL--LALWNP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 IYERWHTPLHICLIWLLTVVALLP-----NFFVGSLEYDPFTYSCTET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 PALSAVLIVTT------AVDVVGNILVTLSV: PNFKLPNAGNLFLVSLALADLVVA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                               ANDALAGETTNINEÖKETTKSTITSBUBUNGE
                                                                                                                                                                                                                                                                                                                                                                              EGNELTYTTILLUGGYGI PLALTINGYEFTELBISFBKUMVEFABGGBGKKAKGSKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVENITATAINRYCYICHSMAYHR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTOPASLSSTIFLIVAYSTMLAVGLVGNTOLVVVITEQKEMENVTNIFIVNLSOSDILVO
                                                                                                                                                                                                                                                                                                             ----VNAMLASIV--AAPALGWLPLNVENFLEEWNHEAIPVOGHUAIFSACHLIAMASIC
                                                                                                                                                                                                                                                                                                                                             KPSDLRSFLTMFVVFVIFAICWAPLNCIGLAVAINPQEMAPQIPEGLEVTSYLLAYFNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                              VVR--HSYLAVAVIWIIACEISLPELSENILTNSPEHNLSLPENP--ESCHETCTEQWOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVCLEVITITYTUMORWITGEALOKVIPEVGOMSVIVSIESMVITALERHQITIHPIGWKP 135
                                                                                                                                                                                                                                                                                                                                                                                                          CTASTOMIAAVVVIHELLETAVVSETYLETWV-----TVTOAP----BKAKPESRITI
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                                                                                                                                                                 PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%;
                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 368.5; DB 13
%; Pred. No. 5.3c-22;
64. Mismatches 118.
               Craniata: Vertebrata: Euteleostomi;
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT:
                                                                                                                                                                 PRT:
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PRINTS: PROODUB: 7tm_1; 1.

PRINTS: PROOZAF: SOMATOSTAINK.

PRINTS: PROOZAF: SOMATOSTINE

PRINTS: PROOZAF: SOMATOSTINAR.

PRINTS: PROOZAF: SOMATOSTINAR.

PRINTS: PROOZAF: SOMATOSTINAR.

PRINTS: PROOZAF: HFLIXION PRINTS: UNKNOWN_1.

PROSITE: PSOOOZAF: HFLIXION PRINTS: UNKNOWN_1.
                                                                                                                                                                              OlyMAX1:
OLYMAX1
OLYMAY-1949 (TrEMBLrel. 10, Created)
OL-MAY-1949 (TrEMBLrel. 10, Last sequence update)
OL-JUN-2000 (TrEMBLrel. 14, Last annotation update)
NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR YB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO: IPROOILI6; -.
INTERPRO: IPROOI418; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                               Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei Actinthomorpha; Paracanthopteryqii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                        OAKHXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00237; G_PROTEIN_RECEPTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO: IPROGO611; -
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                                                                                                                                                   Gadus morhua (Atlantic cod)
Arvidsson A.-K., Wraith A., Tonsson-F
"Cloning of a neuropeptide Y/peptide
                                   SEQUENCE FROM N.A.
                                                                NCHI_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                            290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : .
E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.46\ \mathsf{PESRLCLKPSDLRSFLTMFVVFVIFAICWAPLNCIGLAVAINPQEMAPQIPEGLFVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
                                                                                                                                                                                                                                                                                                                                                                                                                               256 KITRLVL-------MVVVVFVLCWMPFYVVQLL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 SGAGSARPSRTPRPPWVAPALSAVLIVTTAVDVVGNLLVILSVLRNRKLRNAGNLELVSL 82
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                                                                                                                                                                                                                                                                                                                                                              ATVNHVSLILSYANSCANPILYGFLSDNFRRFFQRVL/CL----RCCLLEGAGGAEEEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSCTFIQTASTQYTAAVVVIHFLLPIAVVSFCYLRI-------WVLVLQARRKAK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVHPLR-AATYRRPSVAKLINLGVWLASLLVTLPIAIFADTRPARGGQAVACNLQWPHPA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVADELEMLSVPEVASSAALRH--WPEGSVLCHAVLSVEGLNMETSVECLTVLSVDRYVA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGPGDARAAG------MVAIQCIYALVCLVGLVGNALVIEVILRYAKMKTATNIYILNI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSAVFV-----VYT---FLLGFLLFVLAIGLCYLLIVGKMRAVALRAGW----QQPPPSEK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICHSMAYHRIYRRWHIPLHICL-IWLLIVVALLP-----NEFVGSLEYDERI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.5%;
28.4%;
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Jonsson-Rylander A.-C., La
//peptide YY receptor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.9e-19
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                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DENTA KASADOBURGA ISBORA
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                                                                                                                                                                                                                                                                           374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 388
                     Larhammar D.
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                                                                                                                        Neoteleostel;
   the
   Atlantic
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REPAM; PRO0001; 7tm_1; 1.

PPINTS; PRO0237; GPCPPHONOPSN.

REPINTS; PRO01012; NPPERSINP

REPINTS; PRO1012; NPPERTINFYR

FRINTS; PRO1102; NPPERTINFYR

RESITS; PS01102; NPPERTINFYR

RECEPTOR; NEUTOPEPTIN_PECEPTOR; UNKNOWN_1.

RECEPTOR; NeutoPeptide.
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                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR YC.
                                                                                                                                                                                                                       Eukaryota, Metaroa, Chordata, Craniata, Vortebrata, Euteleostomi, Actinopterygii, Neopterygii, Telcostei, Buteleostei; Ostariophysi Cypriniformes, Cyprinidae, Rasborinae, Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO: IPROUNEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pegul Pept 0.0-0(1998)
EMBL; AF073925; AAD02833.1;
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            MEDLINE=98096393; PubMed=9434780;
Ringvall M., Berglund M.M., Larhammar D.;
                                                                                  subtype in the zebrafish.";
DNA Cell Biol. 16:1357-1363(1997)
                                                                                                 Larhammar D.; "Cloning and characterization of a novel neuropeptide "Cloning".
                                                 SEQUENCE FROM N.A.
                                                                                                                                                      Lundell
                                                                                                                                                                         MEDLINE=98068842; PubMed=9407007;
"Multiplicity of neuropeptide Y receptors: cloning of
                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 LIPIAVVSFCYLRIWVLVLQARP----KAKPFSPLCLKPSDLRSFLTMFVVFVIFAICWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 PLNIFNTVFDWHHELMVSCQHNLIFSVCHLVAMASTCVNPVVYGFLNSNFQKQLKATL-- 335
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13
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RP SEQUENCE FROM N.A.

RC STRAIN-REPKELEY

RX MEDILINE-20196006; PubMed=10731132;

RX MEDILINE-20196006; PubMed=10731132;

RA Adams M D Celniker S F Holt P A Fvans C.A Secayne I.L.

RA Adams M D Celniker S E. Li P.W. Hoskins R.A. Galle R.F. RA Adams M D Celniker S E. Li P.W. Hoskins R.A. Chen L.X.

RA George R A. Lewis S E. Richards S Ashburner M . Henderson S N.

RA George R A. Lewis S E. Richards G. Ashburner M . Chen L.X.

RA George R A. Lewis S E. Richards P C. Champe M . Dfeiffer R.D.

RA George R A. Lewis S E. Richards P C. Champe M . Dfeiffer R.D.

RA George R A. Lewis S E. Helt G. Rampe M . Dfeiffer R.D.

RA Brandon R.G. Rogers Y - H. G. Riaroj R G. Champe M . Dfeiffer R.D.

RA Abrill J.F. Adbayani A . An H - J. Andrews-Pfannkoch C. Raldwin D.,

RA Rallew R.M. Basu A. Baxendale J. Bayraktarcqlu L. Beasley E.M.,

RA Repeson K Y Renos P V Rerman B.D. Bhardari E. Beithakov E.,

RA Rorevoa D. Rottchan M R. Beink B. Brottlor P . Brottlor P.

RA Rorevoa D. Rottchan M R. Beink B. Brottlor P. Brottlor P.

RA Cherry J.M. Cawley S. Dahlke C. Davenport L.B. Davies P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subtype in the zebrafish.")
Riochem Riochys Pos Commun 241-744-755(1847)
EMRL: AF037401 AAAC41277 1. -
ZFIN: ZDB-GEME-990415-175; npyryc.
INTERPRO: IPR000276. -
INTERPRO: IPR000611. -
PPAM: PF00001-74m_1 1
PPAM: PF00001-74m_1 1
PPAM: PF0000277: SPCSFHCDOFSN
                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Elkaryota: Metaroa: Arthropoda: Teceboata: Hexapoda, Isselli.
Pteryoota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidwa: Drosophilidaw: Drosophila
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PROSITE PRO1012; NRPERTIDEYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 HDVIFSACHLTAMASTCVNFVVYGFLNTNFQKELKATL 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PPKAKPESPLCLKPSDLRSFLTMFVVFVI-FAIGWAPLNCIGLAVAINPQEMAPQI
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27.8%;
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                                                      310 SVINFILYAASNENYSVAYYKIFALLKEWGEFLSDMPSRNYHGSKNSKELSGVIFSTFLF 369
                                                                                                                                                               255 EKAPEDNELTYMMYTIFLGELVGFLFT----MIANVVDDERNTSYP-WLHIIASVMAWAS
                                                                                                                                                                                                                     243 KPS--ELRSELTMEVVEVIFAICWAPLNCIGLAVAINPGEMAPGIPEGLEVTSYLLAYEN
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353 IGVQ 356
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                                                                                                         SCLNAIVYGLLNUNFEREYKEI--LLALWN-----FRHCIQDASKGSHAFGLQSPAPPI 352
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97; Conservative
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Search completed: February 18, 2001, 16:46:54 Joh time: 8252 sec

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RESULT 15
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Best Local S
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                                                                                                                                                                  This sequence represents the human neuropeptide Y (NPY) receptor of the invention, designated NPY-77 receptor. The NPY-Y7 receptor can be used for screening and testing (ant)agonists that are useful for detecting changes in receptor activity and which have potential as anti-hypertensive, cardiovascular, anti-psychotic, anti-obesity and anti-diabetic drugs as well as neuronal growth factors. The DNA sequence can be used to produce NPY-Y7 receptor which in turn can be used to identify (ant)agonists of NPY-Y7 receptor, having commercial value as anti-hypertensive, cardiovascular, anti-psychotic, anti-obesity and anti-diabetic drugs as well as neuronal growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding a neuropeptide Y (NPY) receptor useful for screening and testing compounds that detect changes in receptor activity and have potential as e.g. anti-hypertensive and
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                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 14-16; 26pp; English.
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                                                                                                                                      Sequence
              34 LIFTIVVDILGNLLVILSVYRNKKLRNAGNIFVVSLAVADLVVAIYPYPLVLMSIFNNGW 93
                                                                     Local Similarity
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                                                    18.2%; Score 331; DB 21; Length 408; 26.1%; Pred. No. 1.3e-27; ative 76; Mismatches 131; Indels 5
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                                                                                                                          247 FAICWAPINFIGLAVASDPASMVPR----IPEWLFVASYYMAYENSCINAIIYGLINUNF 302
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                                                                                                                                                                                                            198 VPMITVIFCYLRIWILVL-------QVRQRVKPDRKPKLKPQDFRNFVTMFVVFVL 246
344 rrgfqeafqlqlcqkrakpme----aytlkakshvlintsnq1vqes 386
                                        303 FYEVERTI-VSLCTARVFFVFSSNDVADRVKWKESPLMINNVVKVDS 349
                                                                                   286 filswlpl--wtlmmlsdyadlspnelgiiniyiypfahwlafgnssvnpiiyqffnenf 343
                                                                                                                                                                                                                                                                                                                                                                                 94 NLGYLHCQVSGFLMGLSVIGSIFNITGIAINRYCYICHSLKYDKLYSSKNSLCYVLLIWL 153
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Bost Local Similarity 29.2%; Pred. No. 3.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                          Addining the receptors are useful as biological and pharmocological research tools and tor production of antibodies. Agreists of such receptors are useful as analysis: probas directed garlist the unnerare useful for detecting expression of galaninergic receptors, or detecting genetic abnormalities, for diagnosing neurological, conditionated and conditionation of galacting and to detecting and isolating problem of psychiatric disorders and for detecting and isolating neurologic disorders are for detecting and isolating neurologic acid sequences coding for galacinergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New galanin receptor game - useful for diagnosing neurological cardiovascular, endocrine or psychiatric disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8: Page 15-18; 27pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dalanim receptor: gene; antibody; analgesic; probe; detection: 
Hagnosis; neurological disorder; endocrine disorder;
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                                    124 It laumsvdryvaivhstrsselrvstballqvqciwalsiamaspvaybqql-fbpras 182
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                                                                                                                                                                                                                                   2 OGNGSA-LPNASOP-VLRGDGARPSWLASALACVLIFTIV--VDILGNLLVILSVYRNK- 56
SCITEAUSV -----SSAYTIAVVVEHELVEMIIVIECYLEIWILVLQVEQEVKEDEKEKL 229
                                                                 FNITSIAINRYSYISHSIKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTLQYDPRIY 175
                                                                                                                                                      -KLRNAGNIFVVSLAVADLVVAIYPYPIVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSI 115
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Best Local .
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13-00T-1994;
28-DEC-1994;
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116 FNITGIAINRYCYTCHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTLOYDFRIY 175
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17-JUN-1994;
07-CCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane domain, and an NAXXY motif in transmembrane-7, rather than MPXXY. A CYICHS motif, which is a consensus site for cytochrome-c family heme binding, is present in both 1b and 1a-type receptors. The N-terminus contains 1 consensus N-glycosylation site, Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor—antagonists. Agonists may be used in therapy of circudian rhythm disorders such as jet-lag or day-night cycle disorders, to control cyulation, or in alteration of reproductive Cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quanine nucleotide binding proteins (G proteins), with hydrophobic putative transmembrane domains. Unique fea receptors include an NRY motif downstream from the 3rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10: Fig 6; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a novel human high-affinity melatonin-lb receptor (mol.wt. 40,188), which is a membrane protein, coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhythm disorders or reproductive cycles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to screen agonists and antagonists.
                                                                                                                                                                        196
                                      303 KKEYRRIIVSLCIAKVEFVESSNEVALIRVKWKFSF 357
316 rreykrillalwnprhciqdaskgshaeglgspap 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
hes 205: Conserv
                                                                                                                                                                                                                                                                                                                                                                                   65 NIFVYSLAVADLYVAIYPYPLYLMSIFNNGWNLGYLHCQVSGELMGLSVIGSIFNITGIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GNGSALFNASGFYLEGDGARFSWLASALACYLIFTIVVDILGNLLVILSVYRNKKLRNAG 62
                                                                                                                                                                                                                                                                                                                                        niflyslaladlyvafypypillyalfydgwalgeebckasafymglsvigsyfnitaia 135
                                                                               vivifaicwaplnciglaraippgemapgipoglivtsyllayfbselbaivyglingvf 315
                                                                                                                           VEVLEAICWAFLNEIGLAVASDEASMVERIFEWLEVASYIMAYENSCLNAIIYGLLNQNE 202
                                                                                                                                                                    astqytaavvvihfllpiavvstcylriwvlvlgarrkakpesrlclkpsdlrsfltmfv 255
                                                                                                                                                                                                             VSSAYTIAVVVEHELVPMIIVIFCYLRIWILVLQVRQEVKEDEKEKLKEQDERNIVTMEV 242
                                                                                                                                                                                                                                                        inrycyichsmayhriyrrwhtplhicliwlltvvallpnffvgsleydpriysctfiqt 195
                                                                                                                                                                                                                                                                                                 INEYCYICHSLKYDKLYSSKNSICYVLLIWLLTLAAVLENLEAGTLQYDPETYSCTFAQS 182
                                                                                                                                                                                                                                                                                                                                                                                                                            gagsarpsrt-----prppwvapalsavlivttavdvvgnllvilsvlrnrklrnag 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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940S-0261857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.3%; Score 1088; 61.2%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1088; DB 17; Length 362:
Pred. No. 1.1e-109;
L; Mismatches 70; Indels 8
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes peptides (I) binding to galarin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. Y45129 to Y45154 and 195518 to 25552 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 119-121; 153pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides binding to galanin receptor proteins, used to, e.g. improve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
178 rdsnqtfcwehwpnqlhkkayvvctfvfgyllplllicfcyakv---lnhlhkklk-nms 233
                                                                                            176 ···SCIEA·····SVSSANTIAVVVEHELVEMITVIECYLEIWIIVLQVEQEVKEEPP 226
                                                                                                                                                                   117 NITGIAINPYGYJCHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTLQYDPRIY- 175
                                                                                                                               124 tlaamsvdryvaivhsrrssslrvsrnallgvgfiwalsiamasp-----vayyqrlfh 177
                                                                                                                                                                                                                                                                                                                                                    y Match 18.7%; score 340: DB 20: Length 34 Local Similarity 29.3%; Pred No 1.1e-28; hes 96, Conservative 67, Mismatches 123; Indels
                                                                                                                                                                                                                                                                           10 egngsdpeppaeprplfgig·····venfitlvvfglifamgvlgnslvitvlarskpg 63
                                                                                                                                                                                                                                                                                                                2 QGNGS:ALPNASCEVLEGDGARESWLASALACVLIFTIV--VDILGNLLVILSVYRNK-- 56
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                                                                                                                                                                                                    kprsttnlfllplsladlayllfolpfqatvyalptwvlgaflokfihyffftvsm vsif
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Best Local '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating
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                                                                                                                                                                                                                                                                                                                                                                      cannot inhibit adenylyl cyclase activity.
                                                                                                                                                                                                                                                                                                                                                                                       an inhibitor of phosphodiesterase, but unlike the MEL-1Aa protein, it
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206 CYERIWILVEQVRQRVKPDRKPKLKPQDFRNFVTMFVVFVLFAICWAPLNFIGLAVASDP
                                                                  (46 OYVILIMILTIAAVIPNIRAGTIQVDPRIYSCTFAGSVSSAYTIAVVVFHEIVPMIIVIF 205
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                                                                                                                                                                                                             76 IVSUIVACALIEAIAAGITOMETAITSAKENKKEENVONIEAASTIAAVOETAAVIÄEAETAE 88
                             tylaltwilt lialvpattvaslqydprifsetfaqtvsssytltvavahflaplsvatf 210
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                                                                                                     laitqndwtlqnihcqisqflmqlsviqsvfnitaiainrycyichslrydklfnqrstw 150
                                                                                                                                      MSIENNGWNLGYLHCQVSGFLMGLSVIGSIENIIGIAINFYGYIGHSIKYEKIYSSKNSI ]45
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/s 'o- "transmembrane domain 4"
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                                                                                                                                                                                                                                                               68.3%; Grove 1240; DR 18;
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e= "Transmembrane region-VII"
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                                                                                                                                                                                                                                                                                                                                                             "Transmembrane region-II"
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                                                                                                   "Extracellular loop"
                                                                                                                            "Transmembrane region-VI"
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                                                                                                                                                                                                         "Extracellular loop"
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06-JUN-1995;
17-JUN-1994;
07-OCT-1994;
has 7 hydrophobic putative transmembrane domains. The N-terminus has an N-linked glycosylation site typical for G-protein-coupled receptors, and 2 Cys residues in the 1st 2 extracellular loops may form a stabilizing disulfide bond. Pro residues in transmembrane domains IV. V and VI may introduce kinks in the alpha-helices to form of a ligand binding pocket. Phosphorylation sites in the C-tail may be included in receptor regulation primers from the encoding DNA may be used for isolation of sheep, mouse and human receptor sequences. Receptor fragments which interact with
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                                                                                                                                                                                                                         The sequence represents a high-affinity melatonin receptor (mol.wt. 47,424) from Xenopus laevis. The receptor is a membrane protein, coupled to quantine nucleotide binding proteins (G-proteins), and the coupled to demand the coupled to the couple of the coupled to protein the couple of the coupled to the couple of the coupled to the couple of the coupled to the couple of the co
                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
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172..193
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152..171
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                                                                                                                                                                                                                                                                      Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR: mRNA; half-life; skin; amplification; primer, polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase, modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.
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Sequences W25926-7 represent novel allelic Xenopus laevis melatonin receptor MEL-lA proteins. This sequence is a new form of the melatonin receptor designated MEL-lAa, also known as Mel 1-c(alpha). The protein differs from previously known receptors by being 65 amino acids shorter and also having 2 different C-terminal amino acids. The protein is encoded by 2 different alleles (T79083-4) which differ in the 3'
Sequence
                         phosphodiesterase
                                    inhibit adenylyl cyclase, but both proteins can modulate intracellular (MMP), esp. inhibiting its accumulation induced by an inhibitor of
                                                           intranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The coding sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T79057 75. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signalling. MEL-LAA has been shown to
                                                                                                                                                                                                                                              New nucleic acid encoding functional melatonin receptor of Xenopus tor screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melatonin receptor; 3-protein-coupled receptor; glycosylation; disulfide bond, ligand binding pocket; phosphorylation; cytochrome-c family heme binding site; melatonin receptor-agonist; melatonin receptor-agonist; circadian rhythm disorder; jet-lag:
                                                              Region
                                                                                                                                                                                 Region
                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                               Domain
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67..72
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57..68
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16
                                                              132..137
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                               "Butation byto-bromero family home bloding site"
                                                                                                                                                                                                                                                                                                                                                                "Transmembrane region-II"
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                                                                                       "Intracellular loop"
                                                                                                                                                                                                                                                                                                                                                                                                                        "Conserved melatonin receptor motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Transmembrane region-1"
                                                                                                                                                  "Region used to construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Protein-kinase-C phosphorylation site"
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                                                                                                                                                                                                             "Transmembrane region-III"
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17-JUN-1994:
C7-QCT-1994:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
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                                                                     C7-JUN-1995;
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95US-0319887.
94US-0261857.
94US-0319887.
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229..2
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213...2
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202..2
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177..2
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127..1
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105..1;
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66..71
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28..41
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                                                                                                                                                                                                                                      "Transmembrane region-VII"
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                                                                                                                                                                    "Intracellular domain'
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                                                                                                                                                                                                                                      W25926 standard; Protein;
                                                                                                                                     Xenopus melatonin receptor MEL-1Aa
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sequence is given in R88412. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puborty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNA encoding high affinity melatonin receptor one - used to receptor agonists or antagonists e.g. for regulating circadi rhythm disorders or reproductive cycles
Allele; Xenopus laevis; melatonin; receptor, untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling, inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.
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pred No 2 4e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOGNOSALPNASOPVL---RGDGARPSWLASALACVLIFTIVVDILGNLLVILSVYRNKK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNONFEKEYBRIIVSLOTARVEEVDSSNOVADPVXWKPSPLMTNNNVVKVDSV 350
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                                                                                                                                                                                                             /note= "N-qlycosylation site"
/note= "Transmombrane region-169..79
                                                                                                                                                                                                                                                                /moter "N glycosylation site" 23...25
                                                                                                                                                                                                                                                                                           /hote- "Extrac⊷llular domain"
16...18
                         163..182
                                                                                                                                                          80..104
                                                                                                                                                                                     78..83
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                   foot o-
                                                                                                                  /note= "Extracellular loop"
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                                                   . 148
                                                                              . 162

    "Conserved melatonin receptor motif"

            "Tracsmembrane region:IV"
                                    "Butative cytochrome o family heme binding sitto"
                                                                "Intracellular loop"
                                                                                                                                            "Transmembrane region-II"
                                                                                                                                                                                                "Intracellular loop"
                                                                                                                                                                                                                           "Transmembrane region-I"
                                                                                         "Transmembrace region III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1552.5; DB 17; Length 353;
; Pred No 4.8e-160;
28; Mismatches 28; Indels 3;
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17-JUN-1994;
07-CCT-1994;
                                                                                                                                                                                                                                                                                                                           cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                  receptor, which is a membrane protein, employed to granine nucleotide binding proteins (G-proteins), with 7 hydrophobic putative transmembrane Jamains — Receptor fragments which interact with melatonin, or specific annibodies, may be used as receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circulation of disorders such as jet-tag or day-night could disorders such as jet-tag or day-night could disorders such as jet-tag or day-night.
                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     וולישים זוח
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhythm disorders or reproductive cycles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a sheep high affinity melatonin-la
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Local Similarity 81.3%;
hos 287; Conservative 20
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                                                                                                 LPNAGNIEVVSLAVADELVVAIYPYPEVEMSIENNGWNEGYEHOQVSGEHMGLSVIGSIEN 117
                                                                                                                                                                                          CONG-SALFNASQPVL-PODGA--PESWLASALACVLIFTIVVITICANILATI SVYPNKK
               TEARSVASAYTIAVVVEHELVEMIIVIESYCEIWIIVIEVEAKVKESEKEKEKEKSSSES
                                        TTGTATUPYCYTCHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPULPAGTLQYDPRIYSC
366 AA;
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94US-0261857.
94US-0319887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Intracellular domain"
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                                                                                                                                                                                                                          ; Score 1505; DB 17;
; Pred. No. 7.1e-155;
2°; Mismatches 33;
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                                                                                                                                                                                                                                                       DB 17:
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Matches 297
                                                                                                                                                                                                                                     activators are useful for treating circadian rhythm disorders in humans (e.g. jet lag, sleep-wake disturbances in the blind or regulation of ovarian cyclicity) and for control of the reproductive cycle in seasonally breeding animals, while those that are inhibitors are used to control initiation and timing of subcrty in humans. Screening for (A) can now be done in cultures of transformed cells which do not naturally express the receptor (which is naturally localised to a few specific sites in the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising melatonin la receptor promoter and reporter gene - used to transform cells for screening for agents that alter transcription from promoter, e.g. for correcting circadian rhythm disorders or controlling reproduction in animals
                                                                                                                                                                                                                                                                                                                                                           receptor gene promoter (see V04644) linked to a reporter gene. Cells containing (I) are used to screen compounds (A) for abil to alter transcription from the promoter (claimed). (A) that
                                                                                                                                                                                                                                                                                                                                                                                                                       This protein comprises the mouse melatonin la (Mella) receptor, of G-protein coupled receptor that specifically binds melatonin and signals the melatonin-mediated cascade of biological events. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 32: 46pp: English
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                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           claimed nucleic acid (I) comprises a functional melatonin la
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mkgnvsollnatgqapggggggggprpswlastlafiliftivvdilgpilvilsvgrpkk 60
                                                                                      MQGNGSALPNASQPVL---FGTGARESWLASALACVLIFTIVVDILGNLLV1LSVYFNKK 57
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                                                                                                                      al Similarity
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/note= "transmembrane region III"
135. 137
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278..298
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/got⊷= "*ransmemt:ane region IV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= VII
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                                                                                                                                 Score 1570.5; DB 19; Length 353; Pred, No. 5 46-162;
                                                                                                                      Mismatches
                                                                                                                    25) Indels
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17-JUN-1994;
07-00T-1994;
                                            The sequence represents a mouse high-affinity melatonin-la receptor which is a membrane protein, coupled to quantum nucleotide binding proteins (G-proteins). Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circudian phythm disorders such as jut lay if day night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breading animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may alse be expressed in a transgenic animal for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty;
Sequence
                               as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                  Claim 9; Fig 3; 115pp; English.
                                                                                                                                                                                                                                                                    rhythm
                                                                                                                                                                                                                                                                                      ENA encoding high affinity mejatonin receptor one - \alpha receptor agonists or antagonists e.g. for regulating
                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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Best Local 9
Examples: Fig 2: 24pp: English
                                                         N-PSDB: X05747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mental confusion.
                      human melatonin receptor proteins and adonists and antagonists
                                 New melatonin receptor expression cells - useful for screening
                                                                                             Коча J. Shirono H.
                                                                                                                    (JCRP-) JCR PHARM CO LTD
                                                                                                                                             19-JUN-1997;
                                                                                                                                                                                                                   EF:892046-A2
                                                                                                                                                                                                                                                      Misc-difterence 274
                                                                                                                                                                                                                                                                             Misc-difterence 249
                                                                                                                                                                                                                                                                                                                                       Molatonin receptor; mel-la; human; screening; hormone,
                                                                                                                                                                                                                                                                                                                                                             Human melatonin receptor protein mel-la
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                                                                                                                                                                     19-JUN-1998;
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                                                                                                                                             97JP-0180537
                                                                                                                                                                     98EP-0111352.
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                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                             Yokoyama
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This represents a human melatonin receptor mel-la. The invention provides materials for screening for a substance showing affinity for a melatonin receptor protein, which comparises an admal cell containing an expression plasmid for the gene encoding a human melatonin receptor protein. The cells are useful for screening for human melatonin receptor proteins and its agonist or antagonist e g hormouse and synthetic compounds, by measuring changes in metabolic activity. The recembleant human melatonin receptor protein is useful as it has the same activity as natural human melatonin receptor protein. The new screening metabolic better than prior art radioimmunoassay techniques at quantitatively determining melatonin, which uses antibodies produced by linking
                                                                                                                                                                                                                                        Melatonin la receptor; Mella gene; circadian rhythm; puberty; reproductive cycle; jet lag; mouse; G-protein compled receptor
                                                                                                                                                                                                                                                                                                                                                        W23958;
                                              Region
                                                                                             Region
                                                                                                                             Modified-site
                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                         Mouse melatonin la receptor.
                                                                                                                                                                                                                                                                                                                       06-JUL-1998 (first entry)
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                                                                                                                                                           Modified-site
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                                             /note= "Asn is N-glycosylated"
31.55
7.label= I
7.note= "transmembrane region I"
66 91
                                                                                                                                                           Location/Qualifiers
/label= II
/note= "transmembrane region I1"
106..124
                                                                                                                           /note= "Asn is N-glycosylated" 10...12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 F9: Score 1908: EB 20: Congth 350: 99 49: Pred No le-187;
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Region

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receptor, which is a membrane protein, coupled to guantine
C nucleotide binding proteins (6-proteins), with 7 hydrophobic
C purative transmembrane domains. A practial sequence is given in
C R88411. The N-terminus contains 2 consensus N-glycosylation sites,
C compared to 1 site in the Xenopus receptor (R88409), and the
C-terminal tail is 65 amino acids shorter. Receptor fragments which
C interact with melatonin, or specific antibodies, may be used as
C receptor agonists or receptor aniagonists. Agonists may be used
C in therapy of circadian rhythm disorders such as jet-lag or
C day-night cycle disorders, to control cycledian animals. Antagonists
CC may be used to control the initiation or timing of puberty in
CC numans. The receptor gone may also be expressed in a transgenic
CC animal for use as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
17-JUN-1994;
07-OCT-1994;
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 5; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                          DNA encoding high affinity melatonin receptor one – used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
                                                                                                                                                                                                                                                                                                                     The sequence represents a human high-affinity melatonin-la
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                                           Local Similarity
1 MQGNGSALPNASQPVLRGDGARPSWLASALACVLLETIVVDILGNLLVILSVYRNKKLRN 60
                                                                                                   350 AA
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0319887
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94US-0261857.
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274..2
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147..1
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103..121
                                        100.0%; Score 1815; DB 17; 100.0%; Pred. No. 1.7e-188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Putative cytochrome-c family heme binding site"
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                            0: Mismatches
                             C
                            Indels
                                                     Length 350
                            0:
                            Gaps
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This sequence represents the human melatonin receptor protein. The DNA encoding this sequence is used in an expression vector designated pAKKO-hMeIR7. The expression vector is used to produce the chinese hamster ovary (CHO) cells of the invention. The CHO cells express the human melatonin receptor protein, and can be used to identify compounds (such as agonists and antagonists) having affinity to the receptor. The CHO cells can also be used to produce the receptor. The melatonin receptor agonist can be used as an agent for preventing or treating jet lay. Sleeplessness, seasonal melancholia, Alzheimer's disease, dementia caused by cerebral thrombosis, various diseases accompanying ageing, high blood pressure, cancer, and glaucoma. The melatonin receptor antagonist can be used as an ovulation regulator. The melatonin receptor antagonist can be used as an ovulation regulator.

Claim 2; Page 16; 21pp; Japanese.

used as an agent for preventing or treating melancholia, neurosis,

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                                                                                                                                                                                                                    Recombinant human melatonin receptor protein and (ant)agonists used for treating jet lag, Alzheimer's disease, melancholia,
                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melatonin receptor protcin; human; chinese hamster ovary cell: CHO cell; jet lay, sleeplessness; seasonal melancholia; Alzheimer's disease; dementia; cerebrai thrombosis; high blood pressure; cancer; melancholia; ovulation regulator; neurosis; mental confusion: glaucoma; therapy.
                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                   26-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                   JP09084581-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melatonin receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W15786;
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Maximum Match 100%
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GenCore version 4 5 GenCore version 4 5
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High-affinity mela	R89409	17		69.5	1244	
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Human melatonin re	W94761	20		99.5	1808	
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2: /cqn2_6/ptodata/2/iaa/5B_COMB Pep:*
3: /cqn2_6/ptodata/2/iaa/9CTUS_COMB Pep:*
4: /cqn2_6/ptodata/2/iaa/9CTUS_COMB Pep:*
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Copyright (c) 1993 - 2000 compugen Ltd.
US-08-466-103A-2

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US-08-466-103A-18

US-08-451-103A-18

US-08-513-974B-34

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US-08-513-974B-34

US-08-513-974B-34

US-08-673-974B-34

US-08-454-552-3

US-08-454-552-3

US-08-454-552-3

US-08-149-U93A-5

US-08-149-U93A-5

US-08-149-U93A-5

US-08-149-U93A-5

US-08-149-U93A-5

US-08-149-U93A-5

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US-08-896-365-6

US-08-280-365-2

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Sequence 12, Application US/08466103A

Sequence 12, Application US/08466103A

Patent NO. 5856124

APPLICANT: Reppert, Steven M.
APPLICANT: Ebisawa, Takashi
APPLICANT: EDISawa, Takashi
ITILE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: PRECEPTORS AND USES THEREOF
NUMBER OF SECURICES. 29

COFFERS/NOMENCE ADDRESS:
ADDRESSEE Fish & Richardson P.C.
STREET: 225 Franklin Street
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FILING DAIL.

CLASSIFICATION: 430
PEIGE AFFLICATION DATA.

APPLICATION NUMBER: 08/319,887
FILING DATE: 07-0CT-1994
PPIGE APPLICATION NUMBER: 08/251,857
AFFLICATION NUMBER: 08/251,857
AFFLICATION NUMBER: 17-JUN-1994
                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5979
TELEPAX: 617/542-8906
INFORMATION FOR SEQ IN NO. 12:
SEQUENCE CHAPACTERISTICS:
LENGTH: 350 amino acids
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MEDIUM TYPE: Diskett
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PCT-US-410358-8
US-08-454-549-4
US-08-454-552-4
US-08-456-552-3
US-07-783-602C-1
US-08-16-194-338-7
US-08-467-5-78-10
US-08-351-473B-4
US-08-351-473B-4
US-08-10-93A-6
US-08-11-245-6
US-09-11-245-6
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Patent No. 5939264
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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APPLICANT: Tugdle, Chrisoper K.
APPLICANT: Messer, Lori A.
APPLICANT: Tun-Ping, Yu
APPLICANT: TANANT ARRESS IN ANIMALS
NUMBER OF SEQUENCES: 25
**CHRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 515-288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Hold S.
PEGISTRATION NUMBER: 37,710
PEFEKENCE: [he, NFT NUMBER: ST
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PRIOR APPLICATION DATA:
MOLECULE LYPE: peptide
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DEFRATING SYSTEM: PC-COS/MS-COS
SOFTWARE: Patenth Release #1.0, Version #1.30
STREET APPLICATION DATA:
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    Mismatches

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                                                                                                                       APPLICATION NUMBER: 60/022/185
EILING DATE: 18-JUL-1996
AITORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 1 BLAINEYCYICHSLKYEKLYSSKNSECYVELIWELILAAVEFREKAGIEGYDPRIYSC 177
NAME: Fraser, Janis K.
KEGISIKATION NUMBER: 34
KEFEFENCE/PROTET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows SOFTWARP:
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                                                                                                                                                                                                                                                                         FILING DATE:
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MELATONIN 1A RECEPTOR GENE
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MOLECULE TYPE:
FRAGMENT TYPE:
US-09-290-420-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
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                                                                                                                                                                                                                                         COUNTRY: US
21F. 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                     OPERATING SYSTEM. Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURPENT APPLICATION DATA:
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ADDRESSEE: Fish & Richardson P.C.
STREET. 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reppert, Steven M. APPLICANT: Ebisawa, Takashi
PRIOR APPLICATION DATA
                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 07-001 1594
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nes 297, Conserv
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                                                                                                             APPLICATION NUMBER - FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
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internal
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84.1%; Pred. No. 7.9e-124;
ative 28; Mismatches 25; Indels 3; Gaps
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APPLICANT: Reppert, Steven M.
APPLICANT: Ebisawa, Takashi
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REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
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                 OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456 103A
                                                                                                                                     ZIF: C2110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: *RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: $29
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ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
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REGISTRATION NUMBER:
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                                                                                                                COMPUTER:
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                                                                                                                                                                                                                  COUNTRY
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FILING DATE:
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                                                                                                              IBM Compatible
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17-JUN-1994
06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                             Takashi
HIGH-AFFINITY MELATONIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00786/250002
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08896365
Patent No. 5939264
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Best Local s
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                                                                                                                                                         APPLICANT: Rothschild, Max F.
APPLICANT: Tuggle, Chrisopher E.
APPLICANT: Messer, Lori A.
APPLICANT: Messer, Lori A.
APPLICANT: Tun-ping, Yu
TITLE OF INVENTION: REPRESE AND GENETIC MARKERS FOR IMPROVED
TITLE OF INVENTION: REPRESEDUCTIVE TRAITS IN ANIMALS
NUMBER OF SECURINESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MALECULE TYPE: protein FRAGMENT TYPE: internal
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/41 FILING DATE: 07-0CT-1594 FFICK APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TopoLody: liner
Legitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZTR LNUNFRKEYFFIIVSLCTAFVEFVDSSNEVADRVKWKPSFLMINNNVVKVDSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 TEAUSVSSAYTIAVVVEHELVPMIIVIECYLRIWILVLQVRQRVKPDRKPKLKPQDERNE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 ITGIAINKYGGIGHSLKYGKLYSGINSLYVYFLIWILILVAIVPNLGVGILGYDFFIYSG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <14 LNONFROEVEKTIVSTOTTKMEEVESSNHVADRIKEKPSELIANHNLIKVESV 366</p>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #54 VTMFVVFVLFAIGWAPLNFIGLVVASDPASMAPRIPEWLFVASYYMAYFNSGLNAIIYGL 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 TETUSVSSAYTTAVVVEHETVPMLVVVECYLRIWALVLQVRWKVKPDNKPKLKPQDERNE 253
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RECISTRATION NUMBER: 74,819
REPERENCE/FOOTKET NUMBER: 007
                                                CONTRY:
                                                                           STATE:
                                                                                              TITY: Des Moines
                                                                                                                           STREET
                                                                                                                                                 ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 EKNAGNVEVVSLAVADELVAVYPYPLALASIVNNGWSLSSEHCQLSGELMGLSVIGSVES 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LRNAGNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFN 117
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                             50409
                                                                        IOWat
                                                                                                                           HOI Grand Avenue, Suite 4200
                                                ESA.
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Glarity 81.9%; Pred. No. 2.4e-118;
Gaiservative 29; Mismatches 33; Indels
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617/542-8906
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17-JUN-1994
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                                                                                                                                                                              Sequence 6. Application US/08466103A Patent No. 5856124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Rest Local Similarity
Matches 287; Conserv
GENERAL INFORMATION:
APPLICANT: Expect, Steven M.
APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
IITLE OF INVENTION: RECEPTORS AND DESCRIPTIONS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 515-288-3667
TELEPHONE: 515-288-1338
INFORMATION FOR SECULD NO: 7:
SEQUENCE CHARACTERISTICS:
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COMPUTED: IBM PC nompatible
PFFAILUR SYSTEM. PT-108/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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HYPOTHETICAL: r
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NAME: Nebel, Heidi S.
REGISTRATION NUMBER 37,719
REFERENCE/DOCKET NUMBER ISHER 021591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 515-288-3667
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                                                                                                                                                                                                                                                                                                                                                                                          298 LNONFEKEYFFIIVSLOTAEVFEVOSSNOVADEVKWKESPLMINNNVVKVOSV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 VTMFVVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIIYGL 297
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 LRNAGNVEVVSLAVADELVAVYPYPLALASIVNNGWSESSEHCQESGELMGESVIGSVES 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGNG-SALPNASQPVL-RGDGA--RPSWLASALACVLIFTIVVDILGNLLVILSVYRNKK 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEAQSVSSAYTIAVVVFHELVPMIIVIFCYLRIWILVLQVEQBVKPD8KPKLKPQDEBNE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.9%; Score 1505; DR 2; Length 366; diarity 81 3%; Pred No. 2.4e-118; Conservative 29; Mismatches 33; Indels
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ADDRESSEE: Fish & Richardson P.C STREET: 225 Franklin Street CITY: Boston

COUNTRY:

SD WA

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                                                                                                                                                                   US-08-466-103A-2
                                                                                               Sequence 2, Application US/08466103A Patent No. 5856124 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 290;
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INFORMATION FOR SFQ ID NO: 6:
SEQUENCE CHARACTER/STICS:
LENGTH: 288 amino acids
                  APPLICANT: Reppert,
APPLICANT: Ebisawa,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/2
APPLICATION NUMBER: 17-JUN-1994
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               242 VVEVLEATCWARELNETGLAVASDPASMVPRIPEWLFVASYYMAYENSCLNATTYGLLNQN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ATNRYCYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTLQYDPRIYSCTFAQ 181
                                                                                                                                                                                                                                                       240 FRKEYRRIIVSLVTARVFFVDSSNDVADRVKWKPSPIMTNNNVVKVDSV 288
                                                                                                                                                                                                                                                                                                302 FRKEYRRIIVSLCTARVFFYNSSNDVADRVKWKPSPLMTNNNVVKVDSV 350
                                                                                                                                                                                                                                                                                                                                         160 VVEVLEATOWAFLNETSLAVASOPASMVESTPEWLEVASYYMAYENSOLNAITSOYWNON 239
                                                                                                                                                                                                                                                                                                                                                                                                                             120 SVSSAYTIAVVVEHFLVEMIIVIECYLPIWILVLQVPQRVKPDRKPKLKPHDERNEVTMF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 SVSSAYTIAVVVEHELVPMIIVIFCYLFIWILVIQVPQPVKPDRKPKLKPQDFRNFVIMF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/3 FILING DATE: 07-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Similarity 96.9%;
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                                                             Reppert,
Ebisawa,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995
                      RECEPTORS AND USES THEREOF
                                             HIGH-AFFINITY MELATONIN
                                                                                   Steven M.
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                                                                 Takashi
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    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1443.5; DB 2; Length 288; Pred. No. 2.5e-113; Pred. No. 2.5e-113; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
EILING DATE: 07-OCT-11994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
EILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPPESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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CITY: H
331 GGTEGLKSKPSPAVTNNN 348
                                   326 DVADRVKWKPSPLMTNNN 343
                                                                              271 FHVAPKIPEWLFVLSYFMAYFNSCLNAVIYGVLNONFRKEYKRILMSLLIPRLLFLDTSR
                                                                                                               266 ASMVPRIPEWLEVASYYMAYENSCLNALLYGLLNQNEKKEYERITVSLCTARVFFVDSSN 225
                                                                                                                                                         211 CYLRIMVLVIQVKHRVRQDFKQKUTĞIDLRNELIMEVVEVLEAVGMAFLKEISLAVAINE 270
                                                                                                                                                                                                  206 CYLRIWILULQURQRVKPORKPKLKPQDFRNEVIMEVVEVLEAICWAPLNEIGLAVASDF 265
                                                                                                                                                                                                                                            151 CYLGLTWILTIIAIVPNEFVGSLQYDPKIFSC1FAQTVSSSYTIIVVVVHFIVPLSVVTF 210
                                                                                                                                                                                                                                                                      146 CYVLLIWLLTLAAVLPNLRAGTLQYDPRIYSCIFAQSVSSAYTIAVVVFHFLVFMIIVIF 205
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                                                                                                                                                                                                                                                                                                                           91 IAIFQNGWTLGNIHCQISGELMGLSVIGSVENITAIAINRYCYICHSLRYDKIYNOPSTW 150
                                                                                                                                                                                                                                                                                                                                                                86 MSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIAINKYCYICHSLKYDKLYSSKNSL 145
                                                                                                                                                                                                                                                                                                                                                                                                            31 LISALAVVLIFTIVVDVLGNILVILSVLRNĶKLUNAGNLFVVSLSIADLVVAVYPVPVIL 90
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; Sequence 8, Application US/08896365; Patent No. 5939264; CENERAL TANDON:

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REFERENCY/POCKET NUMBER: IST
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3567
TELEPHAX: 515-288-1238
INFORMATION FOR SEQ ID NO: 8:
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APPLICANT:
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AUTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,
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APPLICATION NUMBER: US 60/022, 180
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FITLE OF INVENTION: GENES AND GENETIC MAPKERS FOR IMPROVED
TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS
NUMBER OF SEQUENCES: 25
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DEFAILING SYSTEM: PC-DOS/MS-LOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

"TREENT APPLICATION DATA.
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141 VDSSNHVAHRIKRKESE 257
                                                                                                                                                                                    181 VASEFASMAPRIFEWLFVASYYMRYFNSCHNATTYGLLNQNERQEYRKTIVSHOTTKMFF 240
                                                                                                                                                                                                                                                                          26.1 VASDPASMVPRIPEWLEVASYYMAYENSCHNATTYGITNQNERKEYPRIIVSLCTARVEF 320
                                                                                                                                                                                                                                                                                                                                                                         121 LVVIFCYLRIWALVLQVRWRVKPDNKPKLKPQDFRNEVTMEVVFVLEAICWAPLNEIGLV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 SKNSLCYVLLIWLLTLAAVLPNLRAGTLQYDPRIYSCTFAQSVSSAYTIAVVVFHFLVPM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 STNSLCYVELIMMLTLVAIVPNLCVGTLQYDPRIYSCTFTQSVSAXTIAVVVFHFIVPM 120
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                VDSSNDVADRVKWKPSP 337
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Messer, Lori A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Appl
Patent No. 585612
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 205:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFFLICATION NUMBER 09/261,85
FILING DATE: 17 JUN-1994
ATTORNEY FAGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/POACET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows95
SOFTWARE: FASISED for Windows Version 2.0
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: 18798/4475.108A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: PECEPTOPS AND USES THEREOF
256 VEVIEAICWAPLNCIGLAVAINPOEMAPOIPEGLEVISTELAYENSCLNAIVYGLLNONT TIS
                                        243 VFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIIYGILNQNF 3C2
                                                                                                         163 VSSAMITAVVVEHELVPMITVIECYLKIWILVUČVEGEVKEGEKEKTKEGGFERNEVIMEV 242
                                                                                                                                                                      136 INPYCYICHSMAYHFTYFRWHTFLHICLIWLLTVVALLFNFFVGSLEYDPRIYSCTFIQT 195
                                                                                   196 ASIQYIAAVVVIHELLPIAVVSECYLKIWVLVIQAKKKAKPESKLCIKPSDIRSFLIMEV 255
                                                                                                                                                                                                            123 INEYCYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLKAGTLQYDPRIYSCTFAQS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/3 FILING DATE: 07-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 98,08,466,103A FILING DATE: 06-JUN-1995
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ZIF: 02110-2804
                                                                                                                                                                                                                                                                                                  63 NIEVVSLAVADLVVAIYEYELVLMSIENNGWNLGYLHDQVSGEIMGLSVIGSIENTTGIA 122
                                                                                                                                                                                                                                                                                                                                             24 GAGSAPPSPT------PPPPWVAPALSAVLIVTTAVDVVGNILVIISVIPNPKIPNAG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                         76 NLFLVSLALADLVVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iration 08,08466103A
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                                                                                                                                                                                                                                                                                                                                                                                                                                59 9% Score 1088; DB 2; Length 362;
61.2%; Fred No. 1.4e-83;
ative 52; Mismatches 70; Indels
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303 RKEYRRIIVSLCTARVFEYDSSNDVADPVKWKPSP 337

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US-08-896-365-9
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CELL TYPE: Melanocyte
US-08-896-365-9
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                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tuggle, Chrisopher K. APPLICANT: Messer, Lori A. APPLICANT: Tun-Ping, Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rothschild, Max F. APPLICANT: Tuggle, Chrisopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-JUL-1996 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 60/022,180
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REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 801 Grand CITY: Des Moines STATE: Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                         126 YOYICHSLKYDKLYSSKNSLCYVLLIWLLTLPAVLPNLPAGTLQVDPRIYSCTFAQSVSS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: a
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121 LFAICWAPLNFIGLAVASDPASMAPRIPEWLFV 153
                                   246 LFAICWAPLNFIGLAVASDPASMVPRIPEWLFV 278
                                                                                                                186 AYTTAVYVEHELVEMITVIFOYLETWITVLQVPQPVKPDPKPKLKPQDERNFVTMFVVFV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                 Watch 38.3%; Score 696; DB 2; Length 153; Local Similarity 84.3%; Pred No 2.9e-51; nes 129; Conservative 11; Mismatches 13; Indels
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                                                                           61 AYTIAVVVEHELVEMVIVIFRYLÞIMVLVLQTEMPAKÞENNPRIKÞQDERNEVIMEVVEV 120
                                                                                                                                                      1 YOYICHSLKYDRWYSNRNSIGGVELIGVLTLVAIVTNLGMGTLQYDPPTYSCTFAQSVSS 60
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801 Grand Avenue, Suite 3200
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515-286-1338
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RESULT 12
US-08-513-974B-343
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; Patent No. 6114139
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JF
FILING DATE: 20-JAN-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF
FILING DATE: 28-DEC-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF
APPLICATION NUMBER: JF
EILING DATE: 02-NOV-19
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-2

APPLICATION NUMBER: JP 6-2

FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-1

APPLICATION NUMBER: 11-AUG-1994

FILING DATE: 11-AUG-1994

FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUERENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
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TITLE OF INVENTION: G PROTEIN COUFLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
INFORMATION FOR SEQ ID NO: 343:
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APPLICATION NUMBER:
FILING DATE: 19-AUG-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER.
                                                 REFERENCE/DUCKET NUMBER 45)
TELECOMMUNICATION INFORMATION:
                                                                                                                           FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                      APPLICATION NUMBER. JF 6
FILING DATE: 11-AUG-1945
               TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                         NAME: Resnick, David S
REGISTRATION NUMBER: 34
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Fujii, Ryo
Ohtaki, Tetsuya
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14-SEP-1995
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28-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/TP45/01544
FILING DATE: 10-AUG-1995
                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPHRATING SYSTEM: PC-DOS/MS-TOS
SOFTWARE: Fatentin Resease #1.0, Vers.of. #1.00
'CTRRENT APPLICATION DATA:
'CTRICKTON' FORMERS. DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ohdi, Kazuhiró
TITLE OF INVENTION: O PROTEIN COUPLED RECEPTOR PROTEIN.
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chtaki, Tetsuja
APPLICANT: Pukusumi, Shoji
APPLICANT: Ohqi, Kazuhiro
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 SYYMAYENSCLNAIIYGLLNONERKEYRFI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 MSKKSFASKKKTAQTVLVVVVVPOTSWLPHHVVHLWAFFOAFPLTPASFFFFFI-----T 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 FHRDSNQTFCWEQWPNKLHKKAYVVCTFVFGYLLPLLLICFCYAKV---LNHLHKKLK-N 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 YSTIFACSV------SSAYTIAVVVEHELVEMITVIFCYLEIWILVLQVEQPVKEE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 IFNITGIAINRYCYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTLQYDPRI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 AHCLAYSNSSVNPITYAFISENFPKAYKOV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 RKPKLKPQDFRNFVTMFVVFVLFAICWAPLNFIGL-----AVASDPASMVPRIPEWLFVA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARRESPONDENCE ADDRESS: ACCESSION, ROBERTS & CUSHMAN, LLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 18 6%; Shore 337.5; DB 3; Length 349;
Local Similarity 28.2%; Pred. No. 5.5e-21;
hos 93; Conservative 68; Mismatches 124; Indels 45; Gaps
                                                                                                                             CLASSIFICATION:
                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                           02109
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Fujii, Ryo
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  JP 7-093989
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PRIOR APPLICATION DATA.
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PPIOP APPLICATION NATA:
APPLICATION NUMBER: JF 6-189272
ETILING DATE: 11-AUG-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.5%; Score 335.5; DR 3: Longth 348; Bost Local Similarity 29.2%; Prod No 8e-21; Matches 93; Conservative 68; Mismatches 124; Indels 45; Gaps
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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PPTOR APPLICATION DATA:
APPLICATION NUMBER: JP 6:
FILING DATE: 11-AUG-1994
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PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 6-236357
FILING DATE: 70-SEP-1994
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APPLICATION NUMBER
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287 AHCLAYSUSSUNPITYAFLSENFFKAYKQV 316
                                                                                                                                                                                                  177
                                                                                                                                                                                                                                                                                                      123 IFTLAAMSVURYVAIVHSRESSIRVSENALIGVGFIWALSIAMASP------VAYHORL 176
                                                 280 SYYMAYENSCLNAIIYGIJ.NQNERKEYRRI 309
                                                                                                                                                                                                                                                       175 YSCTFAQSV-----SSAYTIAVVVEHELVEMIIVIECYLKIWILVIQVRQRVKED 224
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                                                                                                                                                                                                                                                                                                                                                                                                        63 PGKPESTINLEILNLSIAFLAYII.FCIPFQATVYALPTWVLGAFICKEIHVFETVSMI.VS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 **ELEMABHIFVVSLAVARI VVA TYDYDLVI MSTEWRRWH DYCHOLVSOFIMOLSVIGS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QGNGSALPNASQPVLR---GIGARPSWLASALACVLIFTIV--VDILGNLLVILSVYRNK 56
                                                                                              MSKKSEASKKIAQIVLVVVVVFGISWLPHHVVHLWAFFGAFPLIPASFFFRI-
                                                                                                                                                RKPKLKPQDERNEVIMEVVEVLEAICWARELNEIGL ---- AVASDRASMVPRIREWLEVA 279
                                                                                                                                                                                                  EHEDSNUTECWEGWENKLHKKAYVVOTEVEGYLLELLLIGEGYAFV - - LNHLHKKLK N 202
                                                                                                                                                                                                                                                                                                                                                      IENITGIAINEYCYICHSUKYDKLYSSKNSUCYVILIWUUTIAAVI-PNI.RACTIQYDERI 174
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US-08-513-974B-344
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APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii. Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Ohtaki, Shoji
APPLICANT: Ohqi, Kazuhiro
TITLE OF INVENTION: G. PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION UNMRER: 1P 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
                                                     REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INCREMATION
TELEPHONE: 617-523-3400
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                                                                                                                                                   APPLICATION NUMBER: JP 6
FILING DATE: 11-AUG-1994
ATTORNEY ABENT INFOEMATION:
                                                                                                                                                                                                                 FILING DATE: 11-AUG-1945
PRICE APPLICATION DATA:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 6
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: JP 6-236357
APPLICATION DATA
PRIOR APPLICATION DATA
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-
FILING DATE: 02-NOV-1994
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FILING DATE: 16-MAR-1995
FRIGH APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRICH APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                    TELEPHONE: 617-52:
TELEPHONE: 617-523-6440
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SCETWARE FatentIn Felessor #1 ) Version #1
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IBM FC compati
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11-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6114139
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 3 EPOTEIN COGGLED RESTRETOR PROTEIN, TITLE OF INVENTION: PRODUCTION, AND USE THEREOF NUMBER OF SEQUENCES: 380 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinuma, Shu
APPLICANT: Hosoya, Mas
APPLICANT: Fujii, Ryo
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                                                                    CLASSIFICATION: 536

EPIOP APPLICATION DATA:
ALLICALJON COMMER: 101, 2005, 01509

FILING DATE: 10-AUG-1995
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                         PRIOR APPLICATION DATA: APPLICATION NUMBER: .
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERAIING SYSIEM: PC-1.55,MS-1.0S
SOFTWAKE: Patentin Release #1.0. Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 SOTEAQSV-----SSAYTIAVVVEHELVEMIIVIFOYLEIWII VIQVEQEVKEGERRI 229
                                                                                                                                                           APPLICATION NUMBER FILING DATE: 14-SE
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ZIP: UZ1U9
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                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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Fukusumi, Shoji
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UMBER: JP 7-093989
19-AUG-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 15-MAR-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177

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MCLECULE TYPE: protein:
US-08-513-974B-342
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TELECOMMONICATION INFORMATION:
TELEPHONE: 617-523-3400
INF-MATION FOR SED ID NO: 442:
SEQUENCE CHARACTERISTICS:
CENGTH: 348 amino acids
TYPE: amino acid
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PHEOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP 194
PHEOR APPLICATION NUMBER: JP 6-189274
PHEOR APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-194
PHEOR APPLICATION NUMBER: JP 6-189273
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PHEOR APPLICATION NUMBER: JP 6-189272
APPLICATION NUMBER: JP 6-189272
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-194
ATTORNETY/ACENT INFORMATION:
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ASPLICATION NUMBER: JP 6-
FILING DATE: 28-DEC-1004
FRIOR ASST.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: J
FILING DATE: 30-SEP-1
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APPLICATION NUMBER:
197 ABCLAYSNSSVNPITYAFLSENFRKAYKQV 316
                                                 240 SYYMAYENSCLNAIIYGLLNQNERKEYRRI 309
                                                                                                           LAA MSKKAEAAKKKTAOTVLVVVVVFGISWLPHHVVHLWAREGAFPLTPASFFERIAAAA 286
                                                                                                                                                               225 RKPKLKPODERNEVTMEVVEVLEAICWAPLNEIGL----AVASDPASMVPRIPEWLEVA 279
                                                                                                                                                                                                                                                                          [75 YSCTFA@SV------SSAYTIAVVVFHFLVPMIIVIFGYLRIWILVL@VR@RVKPD 224
                                                                                                                                                                                                                                                                                                                                    1.14 IFTLAAMSVDRYVAIVHSRRSSSLRVSRNALLGVGFIWALSIAMASP-----VAYHQRL 176
                                                                                                                                                                                                                                                                                                                                                                                     115 IFNITSIAINKYTYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTEQYDPRI 174
                                                                                                                                                                                                                      177 EHROSNOTEOWEOWENKLHKKAYVVOTEVEGYLLELLI I CECYAKV---I NHLHKKI K-N. 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 -- KIRNAGNIEVVSI AVADLVVALYPYPLVLMSIENNÖWNLGYLHOOVSGELMGLSVIGS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Resnick, David S. FEGISTRATION NUMBER: 34,235
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28-DEC-1994
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Search completed: February 18, 2001, 16:49:54 Job time: 8328 sec

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gb_ov.XLU67880
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9b_ov:AF156262
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gb_pat(:AR026631
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qb_ro.PSU14110
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qb_htg23:AP002371
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Query length: 350
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Database length: -1736092196
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-DB-GEREMb1 -OFMI-EASKAP -SUFFIX-rge -GAPOP-12 000 -GAPEXT-4 000
-MINMATCH-0.100 - LOOPCL-0 000 -LOOPEXT-0 000 -GAPOP-4 000
-GAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-F3APEXT-7.000 -XGAPOP-10.000 -XGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -STAPT-1 -MAXPRIX-b10-sum62 -TRANS-humman40.0d1
-LIST-45 -DOGALIGN-200 -THP_SCOPE-pot -THP_MAX-100 -THP_MIN-0
-ALIGN-15 -MODE-LOCAL -OUTFMIT-F15 -MODE-CAPACA -MINLEN-2
-MAXKIBN-2000000000 -USEP-FS0025045 30001_14746 -NCPU-6
-IOPU-3 -LONGLOG -NO_XLPXY -WAIT -THREADS-1
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1105 | U25341 Human Mellb-melatonin r

1105 | AF025633 Sequence 15 from path

1854 | AB035598 Homo sapiens gene for

169287 | AF025237, Homo sapiens chromd

200596 | AC016891 Homo sapiens chromd

1739 | U52219 Homo sapiens chromd

1739 | AF047639 ovis arise melatonin

1801 | AF047639 ovis arise melatonin

1801 | AF047639 thomo sapiens cusmida

741 | U57555 Phodopus sungorus Mellb

76548 | AF047625 Homo sapiens cusmida
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AF130341 Faiths norregicus mel
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AF026635 Sequence 5 from putes
AF026635 Sequence 3 from patent
U31821 Gailus gallus mel lo m
U31821 Gailus gallus mel lo m
U57873 Xenopus laevis mel lo m
U57880 Xenopus laevis mel lo m
AF026628 Sequence 1 from patent
U57861 Xenopus laevis mel lo m
AF18891 ESIX lusius 25 from Fatent
U57862 Sequence 5 from Fatent
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gb_ov.AF178929
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                 Ratio: 5.186
Percent Similarity 100.000
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                                                                                                                                                                                                                                                                                                                                                                                               Quality: 1815.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reppert, S.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon.9606"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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34 eullePheTh: lleValValAsplieLeudlyAsnLeuLeuVaillieLeu 50
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SGELMGLSVIGSTENITGIAINNYCYTCHSEKKYKKYSKLOVULLIWI DILANO

ENLRAGTIGYDEKTYSCCERAGSVISANY IAVVUTHELVENTIV LICYTERE MODULOVE

GYVKETOKIK KIKPODEENETYNETVEVLEAT WAFLINGI SLAVALS KAGEVISKOPILI

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BSPLMTNINIVKVOSV<sup>*</sup>

257 t
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/protein_id="AAB17720.1"
/db_xref="G01602130"
/translation="M09N9SALPNAS@PVLPGE9A8PSWLASALATVI"=FTTYVIIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 י יוויאס Pattus norvegicus mcl
461 י ייייקאר Sus scrofa melatonin
446 י AFITEBER Oncorbynchus mykiss
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Ratio: 5.186
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                                                                               383 (A) PAGPAGA PARATAANGA TAGTSCTAPATOTAGGAGAGTCTCA 432
                                                                                                                                                                                     167 rLeuGlnTyrAspProArgIleTyrSerCysThrPheAlaGlnSerValS 184
                           483 АТАТЕВЕТЕСТВАСВЕТВВЕСТАТОСТВООДЛАКОСТООВТВОАВВВАЮ 532
                                           151 IleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuArgAlaGlyTh 167
                                                                                                                                                           117 nIleThrGlyIleAlaIleAsnArgTyrCysTyrIleCysHisSerLeuL 134
                                                                                                                                                                                                     101 GlnValSerGlyPheLeuMetGlyLeuSerVallleGlySerIlePheAs 117
                                                                                                                                                                                                                                                                                                                                              51 SerValTyrArgAsnLysLysLeuArgAsnAlaGlyAsnIlePheValVa 67
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Sequence 11 from patent US 5856124.
ARC26631
ARC26631.1 GI:5937471
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226 a 223 c 279 g
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                  PREENT: JP 1907C84581-A 1 31-MAR-1997;

TAKEDA CHEM IND LID
OS HOMO Sapiens (human)
PN JP 1997084581-A/1
PD 31-MAR-1997
PF 26-SEP-1995 JP 1995248177
PF 26-SEP-19
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E12945

E12845.1 GI:3251677

JF 1997084581-A/1.
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1 (bases 1 to 1050)

Hinuma.K. Kawamata.V. and Hosova.M. Human MELATONIN RECEPTOR PRODUCTION OF PROTEIN OF RECOMBINANT HUMAN MELATONIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               £12845
Homo sapiens.
                                                                                                                                                                                                                                                                                Homo sapiens (human)
JP 1997084581-A/1
31-MAR-1997
26-SEP-1995 JP 1995248177
HINUMA KUNIJI, KAWAMATA YUJI, HOSOYA MASAKI
C12N5/10,A61F39/04.A61K38/04.A61K38/04 A61K38/04.A61K38/04.E0
    strandedness: Double:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1050 bp
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FEATURES
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rs-09-226-046-12 x F12845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1811.00
Ratio: 5.174
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: E12845 from: 1 to: 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                               201 GAGCTTAGCGGTGGCAGACCTGGTGGTCGCCATTTATCCGTACCCGTTGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 TCATCTTCACCATCGTGGTGGACATCCTSGCCAAACCTTCTGGTCATCCTG
                                                                                                                       251 TOCTGATGTCGATATTTAACAAUGGGTOGAAUCTGGGTTATGTGTACTGC
                                                  401 AGTACGACAAACTGTACAGCAGCAAGAACTCCCCCCTGCTACGTGCTCCTC
                                                                                                                                                                                                              134 ysTyrAspLysLeuTyrSerScrLysAsnSerLeuCysTyrVaiLeuLeu 150
                                                                                                                                                                                                                                                              117 nIleThrGlyIleAlaIleAsnArgTyrCysTyrIleCysHisSerLeuL 134
184 erSerAlaTyrThrileAlaValValValPheHisPheLeuValProMct 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 SerValTyrArgAsnLysLysLeuArgAsnAlaGlyAsnIlePheValVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 cosecacecececececerecreseries ecresseers sectroser 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 | 1SerLeuAlaValAlaAspLeuValValAlaIleTyrProTyrProLeuV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 euIlePheThrIleValValAspIleLeuGlyAsnLeuLeuValIleLeu 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 gGlyAspGlyAlaArgProSerTrpLeuAlaSerAlaLeuAlaCysValL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                        84 alLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisCys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGCAGGGCAACGGCAGCGCGCGCCAACGCCTCCCAGCCCGTGCTCCG 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGGTGTATCGGAACAAGAAGCTTAGGAATGCGGGAAACATCTTTGTGGT 200
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hypothetical: No;
anti-sense: No;
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/db_xref="taxon:9606"
a 310 c 267 g 25
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Gaps: 0
Percent Identity: 99.714
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1. .1050
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REFERENCE
AUTHORS
TITLE
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AUTHORS
                                                                             FEATURES
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                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                     JURNAL
                                                                                                                                                                                                                                                                                                                                                                                                             MELLILINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $1.5°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <17 qValPhoPhoValAspSorSerAsnAspValAlaAspArgValLysTrpL 334</p>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rmetValProArgIleProGluTrpLeuPheValAlaSerTyrTyrMetA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOAGGAATTETGTCACCATGTTGTGTGGTTFTTGTCTTTTTGCCATTTGC 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laTyrPheAsnserCystenAsnAlaIleIleTyrGlyLenLenAsnGln 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lArgClnArgValLysProAspArgLysProLysLeuLysProGlnAspF 234
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014110
                                                                                                                                                                                                                                                                                                                                                                                                             Cloning and characterization of a mammalian melatonin receptor that mediates reproductive and circadian responses Neuron 13 (5), 1177-1185 (1994) 9503323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phodopus sundorus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Cricetinae;
                                                                                                  Boston, MA 02114, USA
On Nov 1, 1555 this se
                                                                                                                                                                Direct Submission
Submitted (29-Aug-1994) Steven M. Reppert, Chronobiology
                                                                                                                                                     Children's Service, Massachusetts General Hospital, 32 Fruit
                                                                                                                                                                                                                                Repport, S.M.
                                                                                                                                                                                                                                                                                                                                Weaver, D.R., Liu, C. and Reppert, S.M.
Nature's knockout: The Mellb melatonin receptor is not necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U14110.1 GI:1554104
                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                        for reproductive an circadian responses in Siberian hamsters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                striped bairy-footed hamster
                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1052)
                                                                                                                                                                                                                                                          (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 388 to 855)
/ordanism="Phodopus sundorus"
/dk_vref="*axon*löö44"
                                                                          Location/Qualifiers
                                                                                                  laws this sequence version replaced 41.50213
                                                                                                                                                                                                                                                        1 to 1052)
                                                     .1062
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alignment_block:
US-09-226-046-12 x FSU14110
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7
                                                                                                               164 gAlaGlyThrLeuGlnTyrAspProArgIleTyrSerCysThrPheAlaG 181
                                                                                                                                                                                                                                                                                                                                             148 ValLeuLeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuAr 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 APPOPTERAGESOLSACATOCATA PETAACAATGCATAGCATOTGGCATAT 300
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AANTORAANTOROGASIAFGATOOOGARAKTEANTORTATAOTIIOAGAT 550
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Patio: 4 720
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/translativd
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/tissue_type="hypothalamus and pituitary pars tuberalis"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 TCTTCAGGTCCGACGGAGGGTGAAACCCGACAGCAAGCCCAGACTGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 LeuclnvalArgGlnArgValLysPrnAspArgLysProLysLeuLysP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 ValProMetIleIleValllePheCysTyrLcuArgIleTrpIleLeuVa 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         801 CCCTGCCACCATGGCCTCCAGGATCCCAGAGTGGCTGTTCGTGGCTAGTT 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 CIGAACCAGAATITCAGACAAGAATACAAAAGAATTCTCGTCTCATTGTT 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 AspSerVal 350
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Fora: A. I. Chdsop: C. Whaver D. P. and Reppert. S. M. Structure, characterization, and expression of the gene encoding the mouse Mella melatonin receptor Endocrinology 137 (8), 3469-3477 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus Mel-la melatonin receptor mRNA, complete cds
                                                                                                                                          Direct Submission Submitted (25-MAR-1996) Steven M. Reppert, Pediatrics.
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U52222.1 GI:1226150
                                                                                                                 Massachusetts General Hospital, Fruit Street, Boston, MA 02114, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
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                                                                      Location/Qualifiers
1. .1503
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/db_xref="taxon:10090"
                                             /organism="Mus musculus"
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                                                                                                                                                                                                                             148 ValLeuLeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuAr 164
                                                                                                                                                                                                                                                                                 401 ACAGCCTCAAGTACGACAAAATATACAGTAACAAGAACICGCTCTGCTAC 450
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                      181 lnSerValSerSerAlaTyrThrIleAlaValValValPheHisPhcLeu 197
                                                                       501 AACCGGAACACTCCAGTACGATCCCCGGGATCTACTACTGTACCTTCACCC 550
                                                                                                                    164 gAlaGiyThrLouGlaTyrAspProArgIleTyrSorCysThrPheAlaG 181
                                                                                                                                                                           451 GIGITCCIGATATCGAIGCIGACACTCATCCCATCATCCCCAAAAAATGAA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ePheValValSerLeuAlaValAlaAspLeuValValAlaIleTyrProT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 laCysValLeuIlePheThrIleValValAspIleLeuGlyAsnLeuLeu 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 LeuHisCysGlnValSerGlyFhcLeuMetGlyLouSorValTloGlySe 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACACTGTCAAGTCAGCGCATTTCTAATGGGCTTGAGTGTCATCGGCTC 350
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Quality: 1570.50
Patio: 4.688
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CQVSAFLMGLSVIGSIFNITGIAMNRYCYICHSLKVOXYEYPLVITSIINNGWNLGYLH
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EWILFVASYYLAXFIKSCLNAIIYGLLNQNFPKEYKKIIVSLCTAKMFFVESSNEEADKI
KCKPSPLIPNNNLIKVDSV"
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Align seq 1/2 to: AR026632
                                   US:09 226:046:12 x AR026632
                                                                                           Percent Similarity: 94.634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTGCCACCATGGTCCCCAGGAICECAGAGTGGCTGTTCGTGGCTAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAGCCAAGATGITCITIGIGGAGAGTTCAAATGAAGAAGCAGATAAGA 1000
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                                                                                                           Quality: 1552.50
Ratio: 4.662
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                                                                                                                                                                                                                                                                                                                                                                              Unclassitied.
                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
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277 c 241 g
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                                                                                                                  pPi-AlaSeiMctValProArgIleProGluTrpLeuFheValAlaSerT 281
                                                                                                                                                                                                                         AlaileCysTrpAlaProLeuAsnPheileGlyLeuAlaValAlaSerAs 254
                                                                                                                                                                                                                                                                                                                                                          LieuSloVulArgSloArgValLysErcAspArgLysErcLysEculysE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                          GIBCCIAIGATTATTATTATTATATATATGGTTCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValProMetIleIleValIlePheCysTyrLeuArgIleTrpIleLeuVa 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-003-1999) to the DDBJ/EMBL/Genbank databases. Takashi
Ebisawa, Saitama Medical School, Dept of Psychiatry; 38 Morchongo,
Moroyama-cho, Iruma-gun, Saitama 350-0495, Japan
(E-mail:tebisawa@saitama-med.ac.jp, Tel:81-492-76-1213,
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/product="melatonin 14 receptor"
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/translation="megagsalpenasoppurglagareswiasilacviltetivvillagareswiasilacviltetivvillagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswiasilagareswias
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                                                                                                                                                                   /gene="hMella"
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Patio: 5.214
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 ValileGlySerIlePheAsnIleThrGlyIleAlaIleAsnArgTyrCy 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 ACCTGGGCTATCTGCACTGCCAAGTCAGTGGGTTTCTTGATGGGCTTGAGC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CATTTATCCGTACCCGTTGGTGCTGATGTCGATATTTAACAACGGGTGGA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 TCAGGAAACATCTTTGTGGTGAGCTTAGCGGTGGCAGACCTGGTGGTGGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 TOGATCCIGGTICTCCAGGTCAGACAGAGGGTGAAACCIGACGGGAAACC 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 TCCACTTCCTCGTCCCCATGATCATAGTCATCTTCTGTTACCTGAGAATA 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 alleTyrProTyrProLeuValLeuMetSerllePheAsnAsnGlyTrpA 94
311 ValSerLeuCysThrAlaArgValPhePheValAspSerSerAsnAspVa 327
                                                                                                                                                                              841 TGTGGCCAGTTACTACATGGCGTATTTCAACAGCTGCC1CAAICCCAITA 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 heValLeuPheAlaIleCysTrpAlaProLeuAsnFheIleGlyLcuAla 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 CAAACTGAAACCACAGGACTTCAGGAATTTTGTCACCATGTTTGTGGTTT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 heHisPheLeuValProMetIleIleValIlePheCysTyrLcuArgIlc 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 snLeuGlyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyLeuSer 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AlaGlyAsnIlePheValValSerLeuAlaValAlaAspLeuValValAl
                                                                                                                            294 lcTyrGlyLeuLcuAsnGlnAsnPheArglysGluTyrArgArgileile 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sThrPheAlaGlnSerValSerSerAlaTyrThrIleAlaValValValP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erLeuCysTyrValLeuLeuIleTrpLeuLeuThrLeuAiaAlaValLeu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACATCTGCCACAGTCTCAAGTACGACAAACTGTACAGCAGCAAGAACT 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCTTCGCCAGTCCGTCAGCTCCCCTACACCATCGCCTTGCTTT 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCAACCTCCGTGCAGGGACTCTCCAGTAGGACCCGAGGATCTACICGTG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cLysLouLysProGlnAspPheArgAsnPheValThrMetPheValValF 244
                                                               eValAlaSerTyrTyrMetAlaTyr®boAsnSerCysI@iAsnAlaIleI 294
                                                                                                                                                                                                                                                                                                          GIGGCCTCTGACCCCGCCAGCATGGTGCCTAGGATCCCGAGAGTGGCTGTT ×40
                                                                                                                                                                                                                                                                                                                                                    ValAlaSerAspProAlaSerMetValProArgIleProGluTrpLeuPh 277
                                                                                                                                                                                                                                                                                                                                                                                                                             TrpileLeuValLeuGlnValArgGlnArgValLysFroAspArgLysFr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOOGGATAGGGTTAAATGGAAAGGTTGTGCACTGATGATGACCAAGAATAATG 1040
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    NOTE: This is a 'working draft' sequence. It currently
    consists of 22 contiqs. The true order of the pieces
    is not known and their order in this sequence record is

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galagan, J., Gardyna, S., Grant, S., Hagos, R., Heaford, A., Horton, E., Howland, J.C., Johnson, R., Jones, G., Kann, L., Karatas, A., Klein, J., Lohoryky, I., Lipe, C., Lorke, K., Mandonald, P., Marquis, N., McEwan, P., McSurk, A., McKernan, K., McLaubhlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Horters, E. F., Elliata, V., Filip, F., Foy, A., Santis, F., Severy, F., Stange-Thoman, N., Stojan-Vich, N., Sakramaniac, A., Talamas, J., Tosfay, S., Tittell, A., Vassillev, H., V., A., Wheelel, J., Ku, X., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, Zhan, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M., Wyman, Zhan, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://trp.doc.or.washiratio.odu/RM/RepeatMasker html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens, clone RP11-45013
Unpublished
2 (bases 1 to 149317)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-NoV-1999) Whitehead Institute/MII Jenter for Jenome Research, 320 Charles Street, Cambildge, MA 02141, USA
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Riffen, B., Linton, L., Nusbaum, C. and Lander, E.
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Center clone name: 45_C_13

Center clone name: 45_C_13

Center clone name: Statistics

Sequencing vector: M13; M77815; 100% of reads

Sequencing vector: M13; M77815; 100% of reads

Chomistry: Dye-terminator B1g Dye; 100% of reads

Chomistry: Dye-terminator B1g Dye; 100% of reads

Chomistry: Dye-terminator B1g Dye; 100% of reads
                                                                                                                                                                                  Insert size: 156000; agarese-fp
Insert size: 147217; sum-of-costigs
Quality coverage: 4.1 in Q20 bases;
Quality coverage: 4.3 in Q20 bases.
                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap: version 0.500731
Consensus quality: 137351 bases at least 040
Consensus quality: 143060 bases at least 030
Consensus quality: 145518 bases at least 020
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Center code: WIRE
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    Genome Center

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    be preserved.

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* runs of N but the warst sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120061 120160, 94F of 100 bp
13766 1 17566; contig of 17346 bp in length
137607 147666; gap of 100 bp
137607 149317; contig of 11711 bp in length
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11626 13650; conti
13651 13750; gap of
13751 15261; wort
15262 15361; gap of
15362 17846; conti
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60555 6786
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10496 11727; contid of
11728 11877
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ผลูลุจ โกสูตรู กก
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7260 8782: co
                                                                                           /note="assembly_fragment"
17947 20355
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          /note="assembly_fragment"
20456. .22520
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15362...17846
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/Clone_lib="RPCI-11 Human Male BAC"
1 7159
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/db_xr-f-"taxon:9606"
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Pontly of 1511 bp in length
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contig of 1823 bp in length
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contig of 1232 bp in length
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of 1513 bp in length
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Ratio: 5.214
Percent Similarity 155.595
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                                                    5125. ACCISSCIAICISCATTSCCAASICASTASSTICSTGATGGSCCTGASC 51211
                                                                                                                                  51160 CTACATOTECCACAGTOTCAAGTACGACAAACTGTACAGCAGCAGCAAGAACT 51111
                                                                                                                                                                                                                                                                                    51210 GTCATCGGCTCCATATTCAACATCACCGGCATCGCCATCAACCGCTACTG 51163
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                                                                                                                                                                                                                                                                                                                         111 ValileGlySerilePheAsnileThrClyTleAlaIleAsnArgTyrCy 127
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                    sThrPheAlaGlnSerValSerSerAlaTyrThrlleAlaValValValP 194
                                                                                                                                                                    erLeuCysTyrValLeuLeuIleTrpLeuLeuThrLeuAlaAlaValLeu 160
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137607, 149317
/note="assembly_frayment
clone_end:T7
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/hote="assembly_fraymont"
105467. .120060
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50610 GTCTCGCTCTGTACAGCCAGGGTGTTCTTTGTGGACAGCTCTAACGACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 TrpIleLeuValLeuGlnValArgGlnArgValLysProAspArgLysPr 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 eValAlaSerTyrTyrMetAlaTyrFheAsnSerCysLeuAsnAlaIleI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 ValSerLeuCysThrAlaArgValPhePheValAspSerSerAsnAspVa 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 ValAlaSerAspProAlaSerMetValProArgIleProGluTrpLeuPh 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 alValLysValAspSerVal 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLYSLOULYSPrOGlnAspPheArqAsnPheValThrM=tPheValValP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leTyrG1yLeuLeuAsnG1nAsnPhcArgLysG1uTyrArgArgI1eI1e 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGU31820 1065 bp mRNA. VPT 10-MAR-10 Gallus gallus Mel-1a melatonin receptor mRNA, complete cds. U31820
                                                                                                           Direct Submission
Submitted (18-JUL-1995) Steven M. Berpert. Lab of Developmental
Chronobiology, Childrens Sve., Massachusetts General Hospital, GRJ
1226, Boston, MA 02114, USA
                                                                                                                                                                                                  2 (bases 1 to 1065)
Reppert, S.M.
                                                                                                                                                                                                                                                                                      Reppert, S.M., Weaver, D.R., Cassone, V.M., Godson, C. and Kolakowski, L.F. Jr.

Melatonin receptors are for the birds: molecular analysis of two receptor subtypes differentially expressed in whick brain
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Futeleostomi; Archosauria; Aves; Meognathee; Galliformes; Phasianidae: Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chicken.
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                                                                                                                                                                                                                                                                   Neuron 15 (5), 1003-1015 (1995)
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="CK A"
                                                                     1. .1065
                                                                                   Location/Qualifiers
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572 ATACAATAGCAGTGGTGTTTTTTCCACTTCATACTTCCCATAGCCATAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 CTAACAGTTGTTGCTATTGTGCCCAACCTGTTGTGGGGATCTCTACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 LeuThrLeuAlaNlaValLeuProAsnLeuArgAlaGlyThrLeuGlnTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 CATTGOTATCAATGGATAGTGCTATATCTGCCACAGTCTGAAATATGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 10 y:\|\phi\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\|\alpha\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 CGCAACAAGAAACTGTGGAAACGTGGGAAATATATTTGTGGTAAGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 CCATCGTGGTGGACCTGCTSGGCAACCTCCTGGTCGTCGGTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 aValAlaAspLeuValValAlaIleTyrProTyrProLeuValLeuMetS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 ArgAsnLysLysLeuArgAsnAlaGlyAsnIlePheValValSerLeuAl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 GOGGGGTGGGGGTGARTFARTTGARTYTAGGGAGGATGATGCTGATGTTGA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 AACGGCACCGTTCTCCCGCGG
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                                                                                                            yrThrileAlaValValPheHisPheLeuValProMetIleIleVal 203
                                                                                                                                                                                                                                                                                                                                     TGACCCCAGGATTTATTCGTCCACATTTGCACAGTCTGTGAGTTCCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hrIleValValAspIleLeuGlyAsnLeuLeuValIleLeuSerValTyr 53
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/rodon_start=1
/product="mel-la melatonin receptor"
/product="mel-la melatoni
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REFERENCE
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                                                                        CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 roLeuMetThrAsnAsnAsnValValLysValAspSerVal 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 672 AGTTANAGGAGAGAAGAAGGGGGATTSAAAAGAAGAGAGTTGAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 eValAspSerSerAsnAspValAlaAspArgValLysTrpLysProSerP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 LysGluTyrArgArgIleIleValSerLeuCysThrAlaArgValPhePh 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   872 ACAGCTGCCTTAATGCCATTATATATGGACTCCTGAATCAGAACTTCAGA 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772 TIGAACTICATTGGCCTTGCTGTGTGTCTTTTACCCAGAAACTATAATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 LeuAsnPheIleGlyLeuAlaValAlaSerAspProAlaSerMetValPr 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heValThrMetPheValValFheValLcuPheAlaIleCysTrpAlaFro 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gValLysProAspArgLysProLysLeuLysProGlnAspFhcArgAsnF 237
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Motazoa; Chordata; Craniata, Vertebrata, Euteleostomi, Munmalia, Eutheria, Cetartiodactyla, Ruminantia; Pecora; Bovoidea; Bovoidea; Caprinae; Ovis.

1 (bases 1 to 1149)
1 (bases 1 to 1149)
Reppert.S.M., Weaver, D.R. and Ebisawa, T.
Clobing and characterization of a mammalian melatomin receptor that mediates reproductive and circadian responses
Neuron 1 (5), 1177-1185 (1994)
                                                                                                                                                                                                                                                            Submitted (29-AUG-1994) Steven M. Children's Service, Massachusetts Boston, MA 02114, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OAU14109 1149 bp mRNA MAOVIS aries Mel-la melatonin receptor mRNA,
                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U14109.1 GI:602131
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                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 1149)
                                                                        /tissue_type="pars tuberalis (pituitary)"
/dev_stage="adult"
49...1149
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                                                                                                                                                                /organism="Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                                                                                  Location/Qualifiers
1. .1149
                         /codon_start=1
                                             /note-"high-affinity receptor"
                                                                                                                                         /sex="male and female"
                                                                                                                                                                                                                                                                                     Reppert, Chronobiology, General Hospital, 32 Fruit St
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alignment_block:
US-09-226-046-12 x OAU14109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 ACAGCCICAGATACGGGAGAAGTTRIAIAMAGGGGAGAATTCCCTCTGCTAC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 isSerLeuLysTyrAspLysLouTyrScrSorLysAsmSerLeuCysTyr 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 rIlePheAsnIleThrGlyIleAlaIleAsnArgTyrCysTyrIleCysH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 CIGCATIGCCAACTIAGIGGCITGCIGAIGGGCITUAALGICAICGGGIC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 CCICCAICCICAICTICACCATCGIGGACATCGIGGGCCAACCICCIG 237
                                                                                                                                                                                                                                                                                                                                        538 GIGIICCIGAICIGGACGCIGACGCICGTGGCGATGGIGATGCCCAACCIGIG 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 CGITTEASCATCACCAGAATTGCCATCAACCGCTATTGCTGCATCTGCC 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 GTTTGTGGTGAGCCTGGCAGTTGCAGACCTAGTGGTGGCCGTGTATCCGT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 lnSerValSerSerAlaTyrThrIleAlaValValValPheHisPheLeu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 yrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyr 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 ValileLeuSerValTyrArqAsnLysLysLeuArqAsnAlaGlyAsnIl 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ArgolyAspolyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 LeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerValIleGlySe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ePheValValSerLeuAlaValAlaAspLeuValValAlaIleTyrProT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 laCysValLeuIlePheThrIleValValAspIleLeuGlyAsnLeuLeu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GlnGlyAsnGly
                                                                                                                                                                                                                 TGTORIGAGGGTGGAGGAGGAGGATCTATTCGTGTACCTTCACGC 637
                                                                                                                                                                                                                                                                        qAlaGlyThrLeuGlnTyrAspProArqIleTyrSerCysThrPheAlaG 181
                                                                                                                                                                                                                                                                                                                                                                                               ValLeuLeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuAr 164
ValFroMetileIleValIlePheCysTyrLeuArgIleTzpIleLeuVa 214
                                                                                          Quality: 1505.00 Patio: 4 533
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VPFCYLRIWALVLQVRWKVKÐNKFKLKPQDERNEVTMEVVEVJEAIGWAÐLNEIGLV
VASDÞASMAÐRIPEWLFVASYYMAYENGCLAAIIYGLLNQNERGEYFKIIVSLGTTKM
EFVDSSMHVAÐRIKKESSÞLIANHLLÍKVDSV'
3 227 C 318 9 278 †
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seq_documentation_block:
Logns AR026624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                               Quality: 1505 00
Ratio: 4.533
Percent Similarity: 94.051
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
                                                                                                                               US-09-225-046-12 x APO25529
                                                                                      Align seg 1/1 to: AR026529 from: 1 to: 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LU38 FACUACCAAGAIGTICTITGTGGATAGCTCCAATCATGTAGCAGATAGAA 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1138 GACTCCGTT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 TCTTCAGGTCAGATGGAAGGTGAAACCGGGACAACAANCCGAAACTGAAGC 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                688 GTTCCGATGCTCGTAGTCGTCTTCTGTTACCTGAGAATCTGGGCCCTGGT 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 roGlnAspPheArgAsnPheValThrMetPheValValPheValLeuPhc 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 alLysTrpLysProSerProLeuMetThrAsnAsnAsnValValLysVal 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 sThrAlaArgValPhePheValAspSerSerAsnAspValAlaAspArgV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     988 CIGAACCAAAFITCAGGCAGGAAFACAGAAAATTAFAGTCTCAFTGTG 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 GCCATTTGCTGGGCTCCTCTGAACTTCATTGGTCTCGTTGTGGCCTCGGA 887
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88 AAGGGAACGGCAGCGGCTGCTGAACGTCTCGCA38AAAAAAAA 137
                           2 GinglyAsnely. .ScrAlaLeuFroAsnAlaSerGinFroValloc... 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Reppert, S.M. and Ebisawa, T.

DNA encoding high-affinity melatonin receptors
Patent: US 5856124-A 3 05-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3 from patent US 5856124. AR026629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.
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                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
327 c 318 g
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Percent Identity: 81.303
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SHE CTGAMCCAMAATTTCAGGCAGGAATACAGAAAAATTATAGTCTCATTGTG 1037
                                                                                                                                                                                                  KJ
E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 rilePheAsnileThrGlyIleAlaIleAsnArqTyrCysTyrIleCysH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 GTITGTGSTSAG NIGSTAGTTGCAGAGCTGGTGGTGGTGTATAGCGT 333
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                                                                                                                                                                                                                                                                HHH COCOMICAGOATGGCACCCAGGATGCCCGAGTGGCTGTTTGTGGCTAGTT 937
                                                                                                                                                                                                                                                                                                                           264 pProAlaSerMetValProArgIleProGluTrpLeuPheValAlaSerT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 AlailoCysTrpAlaProLeuAsnPheileGlyLeuAlaValAlaSerAs 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>4</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 oPhovalValSerLeuAlaValAlaAspLeuValValAlaIleTyrProT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE LOUBLISCYSCINVALSERGLYPheLeuMetGlyLeuSerVallleGlySe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTG/GATGGTGGTAGTGGTTGTGTFA/CFGA/AAT/1/225CCGTGGI 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTOCGTCAGCTCAGCCTACACGA CGCCCCCGGGGGGTGTTCTTCATT KX7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LonAsnGlnAsnPhoArqLysGluTyrArqArqIleIleValSerLeuCy 314
                                                                                                                                   ACTATATGGGATATTTGAAGAGGTGGGTGAATGGGATGATATATGGAGTA 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InserValserSerAlaTyrThrIleAlaValValPheHisPheLeu 197
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                                                                                                                                                                                              yrTyrMetAlaTyrFheAsnSerCysLeuAsnAlaIleIleTyrGlyLeu 297
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
                                                                                                                                                       alignment_block:
US-09-226-046-12 x AF045219
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                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: qb_om:AF045219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                  Quality: 1499.00 Ratio: 4.529 Percent Similarity: 93.768
                                                                                                                Align seg 1/1 to: AF045219 from: 1 to: 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1088 TTAAACGAAACCTTTTCCATTAATAGCCAACCATAACCTAATAAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038 TACCACCAAAATATTATTATATATATATATATCAATCATATATATATAGAA 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 alLysTrpLysProSerProLeuMetThrAsnAsnAsnValValLysVal 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 sThrAlaArgValPhePheValAspSerSerAsnAspValAlaAspArgV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AspSerVal 350
                                      63 AAOGGCAACGGCAGCAGCGCCCCG 112
17 .ArgGlyAspGlyAla
                                                                       2 GlnGlyAsnGly...SerAlaLeuProAsnAlaSerGlnProValLeu..
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Submitted (IR JAN-1998) Whi Endocringle
Rd, Aberdeen AB21 98B, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning and functional analysis of a polymorphic variant ovine Mel la melatonin receptor Biochim. Biophys. Acta 1356 (3), 299-307 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1219)
Barrett, P., Conway, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1219)
Barrett,P., Conway,S. and Morgan,P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostori:
Mammalia; Entheria, Cetarticalactyla, Enninantia, Pecura; Borolica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sheep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                  /rodom_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mote="G-protein coupled receptor; polymorphic variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Ovis aries"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualitiers
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                                                                                                                                                                                                      Dength. 353
Caps: 3
Percent Identity: 81 303
  ArgProSerTrpLeuAlaSerAlaLeuA 31
                                                                                                                                                                                                                                                                                                                                                        330 g
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213 GTGGTCCTGTCCGTGTATCGGAACAAGAAGCTGAGGAACGCAGGGAATGT 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 ACCCCTTGGCGCTGGCGTCTATAGTTAACAATGGGTGGAGCCTGAGCTCC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 GITTGTGGTGAGCCTGGAGTTGCAGACCTGCTGGTGGCCGTGTATCCGT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 isSerLeuLysTyrAspLysLeuTyrSorSerLysAsnSorLeuCysTyr 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 CGTTTTCAGCATCACGGGAATTGCCATCAACCGCTATTGCTGCATCTGCC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 rilePheAsnileThrGlyIleAlaIleAsnArgTyrCysTyrIleCysH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 CIGCATIGCCAACTIAGIGGCIÍCCIGAIGGGCIÍGAGCGICAICGGGIC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 laCysValLeuIlePheThrIleValValAspIleLeuGlyAsnLeuLeu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 TGTGGGGACCCIGCASTATGACCCGAGGATCCATTCCTSTACCTTCACGC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513 GIGITCCTGATCTGGACGCTGACGCTUGIGGGGATCGTGCCCAACCTGTG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ValLeuLeulleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuAr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 ACAGCCTCAGATACGGCAAAGCTGTATAGCGGCACGAATTGCCCTCTGCTAC 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ePheValValSerLeuAlaValAlaAspLeuValValAlaIleTyrPrcT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 ValileLeuSerValTyrArqAsnLysLysLeuArqAsnAlaGlyAsnIl 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 ValProMetileTleValIlePheCysTyrLeuArgIleTrpIleLeuVa 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           613 AGTECGTCAGETCAGECTACACGATEGGEGGTGGTGGTGTTTCCATTTCATA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663 GTTCCGATGCTCGTAGTCGTCTTCTGTTACCTGAGAATCTGGGCCCTGGT 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            753 CCCAGGACTICAGAAATTTIGTCACCATGTTTGTGGGTTTTTGTCCTCTTT 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 rcGlnAspPheArqAsnPheValThrMetPheValValPheValLeuPhe 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              713 TCTTCAGGTCAGATGGAAGGTGAAAAUUGGACAACAAACCGAAACTAAAGC 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 LeuGlnValArqGlnArqValLysProAspArqLysProLysLeuLysF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   863 COCIGACAGCATGGCACCCAGGATCCCCAGTGGCTGTTTTGTGGCTAGTT 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 pProAlaSerMetValProArgIleProGluTrpLeuPheValAlaSerT 281
                                                                                                                                                      953 CTGAACCAAAATTTCAGGCAGGAATACAGAAAAATTATAGTCTCATTGTG 1012
                                                                                                                                                                                                                                                          298 LeuAsnGlnAsnPheArqLysGluTyrArqArqIleIleValSerLeuCy 314
                                                                                                                                                                                                                                                                                                                                                                                        913 ACTATATGGCATATTTCAACAGCTGCCTCAATGGGATCATATATGGACTA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 yrTyrMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeu 297
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                                     sThrAlaArgValFhePheValAspSerSerAsnAspValAlaAspArgV 331
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity.
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                                                                        23 oSerTrpLeuAlaSerAlaLeuAlaCysValLeuIlePheThrIleValV 40
10 AsnAlaSerGlnProValLeu...
                                                                                                                                                    4 AATGUCTUGUNGCAGGCACGAGGGGGGGGGGUNGGGTGGGGGAGAGGGGCC 53
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Mesocricetus auratus melatonin receptor Mella mRNA, partial cds.
AF061158
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Saisonnieres, CNRS-UMR 7518, Universite Louis Pastcur, 12 Rue o
L'Universite, Strasbourg 67000, France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciuregnathi: Mnridae; Cricetinae;
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2 (bases 1 to 977)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesocricetus
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Ratio: 4.750
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/TRANSLATION="LNASQLAFILIFTIVALICATION"
/TRANSLATION="LNASQLAFILIF
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m 255 c 229 g 274 t
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/tissue_type="suprachiasmatic nuclei"
<1. >977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mesocricetus auratus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.679
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নেলুদ্ৰ AF130441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-226-046-12 x AF130341
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                                                          103 TCST98198ACA1eC18888CARCCT8CT8CT8TATATATATATC8C 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                          153 AACAAGAAGCTCAGGAACGCAGGGAATATATTTGTGGCGAGTTTAGCTGT 202
                 88 lePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisCysGlnValSerGly 104
                                                                                              71 lalaAspLeuValValAlaIleTyrProTyrProLeuValLeuMetSerI 88
                                                                                                                                                               38 leValValAspIleLeuGlyAsnLeuLeuValIleLeuSerValTyrArg 54
                                                                                                                                                                                                                                                                                                            53 GCGGCCGTCGIGGCIGGCCICTACACTGGCCTTCATCCTCATCTTTACTA 102
                                                                                                                                                                                                                                                                                                                                                21 aArgProSerTrpLeuAlaSerAlaLeuAlaCysValLeuIlePheThrI 38
                                                                                                                                                                                                                                                                                                                                                                                         3 CLICICAACGOCICICAGCAGGC!CCAGGCGGGGGGGGGGGAAATAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                              8 LeuProAsnAlaSerGlnProValLeuArgGlyAsp......GlyAl 21
Quality: 1459-50
Ratio: 4.723
milarity: 94.785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-FEB-1999) Laboratoire de Neurobiologio Pythmiques et Saisonnieres, CNPS-UMB 7518, 12 Rue de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poirel, V.J., Pevet, P. and Gauer, F.
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/strain="Wistar"
/db_xref-"taxen:10116"
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluTyrArgArgIleIleValSerLeuCysThrAlaArgValPhePheVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAspSerSerAsnAspValAlaAspArg 330
                                                                                                                                                                                                                            Sequence 5 from patent US 5856124. AB025630
1 (bases 1 to 867)
Reppert.S.M. adbisawa,T.
Reppert.S.M. adh-affinity melatonin receptors
DNA encoding high-affinity melatonin receptors
Patent: US 5856124-A 5 05-JAN-1999;
                                                                                                                                                                                                       AR026630.1 GI:5937470
                                                                                                  Unclassified.
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                              Align seg 1/1 to-
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This ENA encodes a human melatonin receptor mel-la. The invention provides matrials for acroning for a subcrate. Showing afficity for a melatonin receptor protein, which conding a number of the part of the gene encoding a human melatonin receptor protein. The cells are useful for screening for human melatonin receptor protein. The cells are useful for screening for human melatonin receptor proteins and its agents to ractioned to be formed as which location and according charges it metabolic activity. The receptor temporal melatonin receptor protein is useful as it has the same activity as natural human melatonin receptor protein. The time streening melatonic section are receptor protein to use streening melatonic before protein the time streening melatonic which uses antibodies produced by linking melatonic which uses antibodies produced by linking
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                                                                                                           rMctValFroArq11eFroGluTrpLeuPheValAlaSerTyrTyrMetA 284
                                                                                                                                                                                                                                                      CAGACAGAGGGTGAAACCTGACCGCAAACCCAAAACTGAAAACGAGACT
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receptor, which is a membrane protein, coupled to quantine including fractions (G-proteins). The gene has been cloned by polymerase chain reaction amplification of human genomic DNA, using protein grave the first the XD-quart laws a probe to obtain clone T0949. Screening of a human hypothalamus xDNA library has resulted in isolation of the full length clone. Primers T0995-56 amplify a 255-bp band of the gene, and have been used with probe T09462 to analyse the tissue distribution of this gene for comparison with the membrane which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-annagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night
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17-JUN-1994:
07-OCT-1994:
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Fireadian rhythm discider, jet leg: day night cycle disorder;
ovulation, reproductive cycle; animal breeding; puberty;
antibody; transgenic animal; drug screening, ds.
                                                                                                                                                                                                                                                                  Claim 8; Fig 5; 115pp; English.
                                                                                                                                                                                                                              The sequence encodes full-length human high-affinity melatonin-la
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Ratio: 5.186
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                                                                                                                                                                                                                                                                                                                                                                                                                             ATATGGCTCCTGACGCTGGCGGCCGTCCTGCTGAACCTCCGTGCAGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qGlyAspGlyAlaArqProSerTrpLeuAlaSerAlaLeuAlaCysValL
                                                         ATCATAGTCATCITCISTIASCISASAATATSSATSCISSTICTCCASGI
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                                                                                                                   IleIleValIlePheCysTyrLeuArgIleTrpIleLeuValLeuGlnVa 217
                                                                                                                                                                                                                                                                                                   TOTOCAGIACGACCOSAGCATOTACTECTSCACCTTCSCCCAGTCCGTCA 582
                                                                                                                                                                                                                                                                                                                                                             rleuGlnTyrAspFrcArgIleTyrSerCysThrFhcAlaGlnSerVals 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuArgAlaGlyTh 167
lArgGlnArgValLysProAspArgLysProLysLeuLysProGlnAspP 234
                                                                                                                                                                                   GCICOGCCTACACCATOGOCGIGGIGGITICOCACTICCIOGICOCCATG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lSerLeuAlaValAlaAspLeuValValAlaIleTyrProTyrProLeuV
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seq_name: /cgn2_2/gcgdata/gcneseq/jcneseqn/NA1997.pat-T60593
X F F F K K X O O O O O O O O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1033 AACCGTCTCCACTGATGACCAACAATAATGTAGTAAAGGTGGACTCCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melatonin receptor protein: human; chinose hamster ovary cell; CHO cell; jet lag; sleeplessness; seasonal melancholia; Alzheimer's disease; dementia; corebral thrombosis; high blood pressure; rancer; melancholia; ovulation regulator; neurosis; mental confusion; glaucoma; therapy; ds.
           This sequence represents the coding sequence for the human melatonin receptor protein. This sequence is used in an expression vector designated pakko-hhotP7. The expression vector is used to produce the chinese hamster ovary (CHO) cells of the invention. The CHO cells express the human melatonin receptor protein, and can be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 heArgAssFheValThrMetFheValValEheValLcuFheAlsTleCyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melatonin receptor protein coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T60593 standard; cDNA; 1050 BP
                                                                                                                                                      Claim 2: Fuge 15, 21pp, Japanese.
                                                                                                                                                                                                   neurosis, etc.
                                                                                                                                                                                                                       Recombinant human melatonin receptor protein and (ant)agonists - used for treating jet lag, Alzheimer's disease, melancholia,
                                                                                                                                                                                                                                                                                                                    WPI; 1997-252999/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1995;
                                                                                                                                                                                                                                                                                              P-PSDB: W15786
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compounds (such as agonists and antagonists) having affinity to

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The CHO cells can also be used to produce the receptor. The mulatonin receptor addist out be used as an agent for preventing or treating jet lag, sleeplessness, seasonal melancholia, Alzheimer's disease, dementia caused by cerebral thrombosis, various diseases arcompanying agentu, high blood pressure, cancer, and glaucoma. The molatonin receptor can also be used as an ovulation regulator. The mulatonin receptor antagonist can be used as an agent for preventing or recating mulatorshells, neurosis, or mental confusion
650 ATCATACTCATCTATTACATCAGAAAATATGAATACTCAGATCTCTCAGGA 650
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seq_name = //ogh__2, grgdata/genesr-p_freesr-pp/NA1946.DAI:v04644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 AACCGTCTCCACTGATGACCAACAATAATGTAGTAAAGGTGGACTCCGTT 1050
                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyA_signal
                                                                                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                       Melatonin la receptor: Mella dene, circadian thythm, puberty
                                                                                                                                                                                                                                                                                                                                                                 Mouse melatonin la receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                           06-.001-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 ysProSerProLeuMetThrAsnAsnAsnValValLysValAspSerVal 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               951 GGTGITETTIGIGGAÇAGCTCTAANGANGANGGATAGGGITAAATGGA 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 gValPhePheValAspSerSerAsnAspValAlaAspArgValLysTrpL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 heArgAsnFheValThrMetFheValValFheValLeuFheAlaIleCys
                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                          reproductive cycle; jet lag: mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGIATTTCAACAGCIGCCTCAATGCCALTALATACGGGCTACTGAACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laTyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeuLeuAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expalationed Ashibeliesly LenaluVaialuserAspiroaluse 267
                       /*tag= f
2356..2796
                                                /*tag= e
/number= 2
2774..2779
                                                                                                  Znotes "base n at position 1477 indicates intron of over 13 kb (full sequence not provide
                                                                                                                                                        /*tag= c
/number= 1
/*tag= g
/note= "(Claim
                                                                                       1487..2796
                                                                                                                                                                                                                              /*tag= .a
/noste= "noste=dides -1142 to -26 (Claim 5)"
                                                                                                                              /*tag=
                                                                                                                                1463..1486
/*tag= d
                                                                                                                                                                                             /note= "contains an intron"
                                                                                                                                                                                                                                                                          Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA: 2796
                                                                                                                                                                                                                        270..2355
                                                                                                                                                                                  270 1462
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WAGG03549-A1

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA sequence comprises the gene coding for mouse melatonic lack (Mella) receptor (see W23958). A 466 by fragment of the gene was cloned from genomic DNA by PCR, and was used to probe a BALB/c adult mouse liver EMRIA SPA/T7 genomic library to isolate the Mella receptor gene. A claimed nucleic acid (I) comprises a functional melatonin la receptor gene promoter (II) linked to a reporter gene. Cells containing (I) are used to screen compounds (A) for ability to alter transcription from (II) (claimed). (A) that are activators are useful for treating circadian rhythm disorders in humans (e.g. jet lag, shere-wake disturbances in the blind or regulation of ovarian cyclicity) and for control of the reproductive cycle in seasonally breeding animals, while those that are inhibitors are used to control initiation and timing of puborty in humans. Screening for (A) can now be done in cultures of transformed cells which do not naturally express the receptor (which is naturally localised to a few specific sites in the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-225-045-12 x V04544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity. 92.798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: V04544 from: 1 to: 2796
                                                                                                                                                                                                                                                                                                                                  1320 CGGCGGGGAGGGAGGAGCGAGGAGGTTGTGGGGTTGTGTGTTGTAGAGTGG 1369
                                                                                                                                                                                                                                                                                                                                                                                                                          1270 ATSAASSCAATSTCASSSAGCTSTTCAATSCACTAASAAGGCTCCAGG 1319
                                                                                                                                            1420 GTCATCCTGTGTGTGTATCGAAAAAAAATTTAGGAAATTAAGGTAGGAGGT469
                                                                                                                                                                                                                                      1370 CCTICATCCTCATCTTTACCATCCTGCACATTCTGGGCAACCTGCTG 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising melatonin la receptor promoter and reporter gene - used to transform cells for screening for agents that alter transcription from promoter, e.g. for correcting circadian rhythm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-120701/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-1998
                                             Claim 4: Page 29-31; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2796 BF; 717 A, 655 C, 649 G, 774 T; 1 other;
                                                                                                                                                                                                                                                                                   31 laCysValLeuIlePMeThrIleValValAspIleLeuGlyAsnLeuLeu 47
                                                                                                                                                                                         48 ValileLeuSerValTyrArgAsnLysLysLouArgAsn
73 spieuValValAlaIleTyrFroTyrFroLeuValLeuMetSerIlePhe 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetGlnGlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeu...
                                                                                                                                                                                                                                                                                                                                                                             .....ArqGlyAspGlyAlaArqFroSerTrpLeuAlaSerAlaLeuA 31
                                                                                       .....AlaGlyAsnIlePheValValSerLeuAlaValAlaA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 1556.50
Ratio: 4.646
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Ferebut likehtity: 82.271
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seq_name: /cgn2_2/gcgdata/geneseg/genesegn/NAluse DAT-TO9951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1970 CCGACAACAAGCCCAAACTGAAGCCCCAGGACTTCAGGAACTTTGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                    2120 CACAGTGGCTGTTCGTGGCTAGTTACTACCTGGCGTACTTCAACAGCTGC 21n9
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                                                                                                                                             2320 CCCAATANTAACTTANTAAAGGTGGACTCTGTT 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2170 CTCAACCCAATTATATACGGACTACTGAATCAGAATTTCAGAAAGGAATA 2219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 leAsnArgTyrCysTyrIleCysHisSerLeuLysTyrAspLysLeuTyr 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 rcAspArgLysPrcLysLeuLysPrcGinAspPheArgAsnPheValThr 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 sTyrLeuArgIleTrpIleLeuValLeuGlnValArgGlnArgValLysP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 LouAsnAlaIleIleTyrClyLeaLouAsnSlnAsnPhoArgLysGluTy (06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 roGluTrpLeuPheValAlaSerTyrTyrMetAlaTyrPheAsnSerCys 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 eIleGlyLeuAlaValAlaSerAspProAlaSerMetValProArgIleP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 AsnAsnGlyTrpAsnLeuGlyTyrLeuHisCysGlnValSerGlyPhele 106
                                                                                                                                                                                                                                                                     340 ThrAsnAsnAsnValValLysValAspSerVal 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 erSerAsnAspValAlaAspArqValLysTrpLysProSerProLeuMet 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 rArgArgIleIleValSerLeuCysThrAlaArgValPhePheValAspS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATCTACTCCTGTACCTTCACCCAGTCTGTCAGCTCAGCGTACACGATA 1 H 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rgIleTyrSerCysThrPheAlaGlnSerValSerSerAlaTyrThrIle 189
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CDNA: 1062 BP

T09951;

1 P - VIII - 1 a.a.e.

(first entry)

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alignment_block
                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                           Transcription polymerase chain reaction amplification of mouse R2-2 mbNA. The curresponding aground that currests of 2 excus divided by a large (over 8 kb) intron. The 3'-untranslated region is 444 bp long, and includes the polyadenylation signal AUUAA. A major transcription start site is located about 100 bp upstream of the initiation coden. Peceptor fragments which interact with cor receptor antaquists. Adonists may be used as receptor-agonists or receptor antaquists. Adonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                                                                                                                                                     US-09 226-046-12 x T09951
                                                                                                                 Align seq 1/1 to: T09951 from: 1 to: 1052
                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06:JUN-1995;
17:JUN-1994;
0"-9CT-1994;
                                                                                                                                                                                                                                                                                                                             Sorphonor 1982 MF: 282 A: 277 C: 241 G: 282 I: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins). The gene has been cloned by reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9: Fig 3; 115pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rhythm disorders or reproductive cycles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding high affinity melatonin receptor one - used to identify receptor amonists or antagenists e.g. for regulating circadian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 1996-05836
P-PSDB: R88413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 - DEC - 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody: transpenic animal; drug screening; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mylatonin receptor-adocist, melatonin receptor antagonist,
circadian rhythm disorder: jet-laq: day-night cycle disorder:
corlation: reproductive cycle; animal preeding: puberty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milatonin-la receptor: mouse: G-protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bigh-affinity melatonin-la receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MASS-) MASSACHUSETTS GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1566 1-NOIC - 13
                                      1 ATHANHAHAATHITAGHAAGHTGCTCAATGCCACTCAGCAGGCTCCAGG 50
                                                                        MetGinGlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeu. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence encodes a mouse high-affinity melatonin-la receptor
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                                                                                                                                                                                                            Quality: 1552.50
Ratio: 4.662
milarity: 94.334
.ArgGlyAspGlyAlaArgProSerTrpLeuAlaSerAlaLeuA 31
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Percent identity: 83.286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 LeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerValIleGlySe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 yrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyr 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 ePheValValSerLeuAlaValAlaAspLeuValValAlaIleTyrProT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lLeuGlnValArgGlnArgValLysProAspArgLysProLysLeuLysF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPORTATION TO THE ATTEMPT OF THE PARTAGE AT A TRANSPORT OF THE PA
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                                                                                                                                                                                                           CIGAATCAGAATTICAGAAAGGAATAGAAAAAAAATTATTOTOCGTTGTG
                                                                                                                                                                                                                                                                                                                             LeuAsnGlnAsnPheArqLysGluTyrArqArqIleIleValSerLeuCy 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTACCIGNANTALITIMAAAAGOTGACTEGAACAATIATATAGGGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yrTyrMetAlaTyrFheAsnSerCysLquAsnAlaIleIlcTyrGlyLcu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
17-JUN-1994;
07-OCT-1994;
                                                                                                                             transcription polymerase chain reaction amplification of sheep pars tuberalls mRNA, using primers derived from the Xenopus laevis melationin receptor sequence (TMO947), and use of the product as a probe on a sheep pars tuberalls cDNA library and a sheep genomic library, to obtain the complete sequence as a hybrid fusion with a 5'-genomic sequence and a 3'-cDNA sequence. Receptor fragments which interact with melations, or specific antibodies, may be used as receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control evaluation, or in alternation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melatonin receptor-agonist, melatonin receptor-antagonist;
circadian rhythm disorder, jet-lag, day-night cycle disorder,
ovulation, reproductive cycle; animal breeding; puberty;
antibody, transgenic animal, drug screening, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High-affinity melatonin-la receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries.
                              reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which is a membrane protein, coupled to quantine nucleotide binding proteins (G-proteins). The gene has been cloned by reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09535320-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence encodes a sheep high-afficity melatonin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Fig 2; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reppert SM:
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for use as a model system to screen agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R88410
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/product= High affinity
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-226-045-12 x T09948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1149 BF; 226 A;
  997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 gAlaGlyThrLeuGlnTyrAspProArgIlcTyrSerCysThrPheAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 isSerLeuLysTyrAspLysLeuTyrSerSerLysAsnSerLeuCysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 CGTTTTCAGCATCACGGGAATTGCCATCAACCGCTATTGCTGCATCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 CISCATISCONACTIACTEGOTICOS GATEGGOTIGAGOGICATOGGGTO 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 GTTTGTGGTGAGCCTGGCAGTTGCAGACCTGGTGGTGGTGGTGIATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 GTGGTGCTGTGCGTGTATCGGAACAAGAAGCTGAGAAACGAAACGCAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 roGlnAspPheArgAsnPhcValThrMetPheValValPheValLeuPhe 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 yrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 VallleLeuSerValTyrArgAsnLysLysLeuArgAsnAlaGlyAsnIl 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 laCysValLeuIlePheThrIleValValAspIleLeuGlyAsnLeuLeu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 .ArgGlyAspGlyAla.....ArgProSerTrpLeuAlaSerAlaLeuA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 AAGGGCAACGCCAGCAGCCCCCTGCTCAACGTCTCGCAGGCGGCGCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 LeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerVallleGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 ePheValValSerLeuAlaValAlaAspLeuValValAlaIleTyrProT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCGGGACGGTGTGCGGCGGGGGGGGTCATHACTGACAAAAAAAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnGlyAsnGly...SerAlaLeuProAsnAlaSerGlnProValLeu..
ValLeuIeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuAr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rIlePheAsnIleThrGlyIleAlaIleAsnArgTyrCysTyrlleCysH 131
                                                                                                      TOTTOAGGTCAGATGGAAGGTGAAAACGAAAAAAAAAAATTGAAGC
                                                                                                                                                      lLeuGlnValArgGlnArgValLysProAspArgLysProLysLcuLysP
                                                                                                                                                                                                               GITCCGATGCTCGTAGTCGTCTTC1GTTACC1GAGAATCTGGGCCCTGGT
                                                                                                                                                                                                                                                               ValProMetileIleValIleFheCysTyrLcuArgIleTrpIlcLcuVa
                                                                                                                                                                                                                                                                                                                        AGTCCGTCAGCTCAGCCTACACCATCGCCGTGGTGGTGTTGCATTTCATA 687
                                                                                                                                                                                                                                                                                                                                                                     InScrValSerScrAlaTyrThrIleAlaValValValPheHisPheLen 197
                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGGGGACCCTGCAGTACGACCCGAGGATCTATTCCTGTACCTTCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGTTCCTGATCTGGACGCTGACGCTCGTGGCGATCGTGCCCAACCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCCTCAGATACGGCAAGCTGTATAGCGGCACGAATTCCCTTCTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCCTTGGCGCTGGCGTCTATAGTTAACAATGGGTGGAGCCTGAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1505 00
4.533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 81.303
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     837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
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seq_documentation_block
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JIIN-1995;
17-JIIN-1994;
07-007-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1188 GACTCCGTT 1146
medatonin-la receptor, which is a membrane protein, coupled
                                                                                                                                            DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders of regulative cycles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Min 19535320-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; transgenic animal; drug screening; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High-affinity melatonin-la receptor gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T09949;
                          The sequence encodes a fragment of a human high-affinity
                                                                                      "Laim 7: Fig 4: 115pp: English
                                                                                                                                                                                                                                                                FEESDAY KR8411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C7 - JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 - DEC - 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melatonin-la receptor; human; G-protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-19949 standard: DNA: 867 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 alLysTrpLysProSerProLeuMetThrAsnAsnAsnValValLysVal 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAR CECCECCAGCATGECACCCAGGATCCCCGAAGTGGCTGTTTGTGGCTAGTI
                                                                                                                                                                                                                                                                                                                                                Reppert SM
                                                                                                                                                                                                                                                                                                                                                                                                   (MASS:) MASSACHUSETTS GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspSerVal 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTANACGCAAACCCICICCAITAATAGCCAAGCATAACCTAATAAAGGTG 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sThrAlaArqValPhePheValAspSerSerAsnAspValAlaAspArqV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAACCAAAATTTCAGGCAGGAATACAGAAAAATTATAGTCTCATTGTG 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAsnGlnAsnPheArqLysGluTyrArqArqIleIleValSerLeuCy 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yrTyrMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pProAlaSerMetValFroArdIleProGluTrpLeuPheValAlaSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCACCAAGATGTTCIIIGIGGAIAGCICCAAICAIGIAGCAGATAGAA 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTATATGGGATAT DECAACAGCIGGCICAATGGGATCATATATGGACTA
                                                                                                                                                                                                                                                                                           1996-058368/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9408-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9585-0319887
9485-0261957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The gene has been cloned by polymerase chain reaction amplification of human genemic (NAA, using primers derived from the Xenopus laevis melatorin receptor sequence (T09947), and use of the product as a probe on a human genome library in plage EMBL 3 under high stringency. The 5'-portion of the gene has been obtained by reprobling the FNA library at low stringency, and the complete sequence is given in T09950. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-antagonists Agonists may be used as receptor-agonists or receptor-antagonists such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aliyo ewa 171 to 189949 from.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-226-046-12 x T09949
                                                                                                                                                                                                                                                                                                                                                                                                                                                            501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 guanine nucleotide binding proteins (G-proteins). The coding sequence corresponds to the region downstream of the first intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 TraggeTATETRACTGCTAAGTCAGTGGGTTTCTFGATGGGGCCTGAGCGTC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 867 BF, 188 A, 242 C; 212 G; 225 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ITATOOGTACOOCIIIGGTGCTGATGTCGATATTTAACAACGGGGTGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 @lyAsnIlePhevalValSerLenAlaValAlaAspLenValValAlaIl 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAACATCTTTGTGGTGAGCTTAGCGGTGACAGAGCIGGTGGCGAT
sLcuLysProGlnAspPheArgAsnPhcValThrMctPhcValValPhcV 245
                                               APOCIGITATION ANTON ANTON ANA AGAINGT GAAD GECAAACCCAA 497
                                                                               CTTCGCCCAGTCGGTCAGCTCGGCCTACACCALCGCGTGGTGGTTTTCC
                                                                                                                                                                                                                                                                                  rPheAlaGlnSerValSerSerAlaTyrThrIleAlaValValValPheH 195
                                                                                                                                                                                                                                                                                                                                                                                                            AssLeuArgAlaGlyThrLeuGlnTyrAspProArgIleTyrSerCysTh 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCTSCCACAGTCTCAAGTGCGACAAACTGTACAGCAGCAAGAACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rIleCysHisSerLeuLysTyrAspLysLeuTyrSerSerLysAbnSerL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eTyrProTyrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnL 95
                                                                                                                                                                                                    isFheLeuValProMetIleIleValIlePheCysTyrLeuArqIleTrp 211
                                                                                                                                                                                                                                                                                                                                                            AACCTCCCCCCATARACTCTCCAACACACACAACATCTACTCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGGCTCCATATTCAACATCACCGGCATCGCCATCAACCGCTACTGTTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ileGlySerTleFheAsmIleThrGlyTleAlaTleAsmArgTyrCysTy 118
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Ratio:
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5.119
97.578
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cod_namo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; ademylyl cyclase;
Claim 1: Page 28-29, 62pp, French
                                                                                                                                                                                                                                                                                                                                                                                                   F-PSDB; W25926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI: 1997-132635/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jockers R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09704094-A1
                                                                                                                                 cardiovascular disease and cancer
                                                                                                                                                                                New nucleic acid encoding functional melatonin receptor of xenopus for screening for potential (ant)agonists useful for e.g. treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ADIR ) ADIR & CIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1996;
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/product= MEL-las receptor protein
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192 lValPheHisPheLeuValProMetTieTleValTiePheCysTyrLcuA 209
                                                                                                                                                                                                                                                                                                                 sequences encode the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from CDNA derived from xenopus skin PNA and amplified using the primers T7945-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEI-laa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-1A. The sequences encode, proteins which are 65 amino acids shorter than those described in the prior art. Also the last 2 C-terminal amino acids encoded by these sequences are different from the previously known proteins. This sequence is a short form of the novel receptor MEL-1Aa also known as Mel 1-c(alpha). As compared to the long form (179065), the difference occurs in the 3 unitranslated region (both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 enserVallleGlySerllePheAsnIleThrGlyIleAlaIleAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GTTGCTGTGTATCCCTATCCGGTATAATTCTCACAASCTATTTTCCACAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 CCTGGGCAATATATTGGTCATTTTGTCTGTCCTGAGGAACAAGAAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1147 BP; 317 A; 234 C; 242 G; 254 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphodiesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 ValAlaIleTyrProTyrProLeuValLeuMetSerIlePheAsnAsnGl 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 rgAsnAlaGlyAsnIlePheValValSerLeuAlaValAlaAspLeuVal 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 eLeuGlyAsnLeuLeuValIleLeuSerValTyrArqAsnLysLysLeuA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 CTCACCTCTGCCCTGGCGGTGGTTGTTATATTCACCATTGT1G1GGAIGI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 LeuAluSerAlaLeuAluCysValLeuIlefheihrileVulVuLAspii 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTrpAsnLeuGlyTy:LeuHiscysGloValSerclyPhoLouMotolyL 109
                                                               TCTTGCACATTTGCGCAGAGAGAGTGAGTTCCTCAIACACCAIAACAGTAGI 590
                                                                                                                    SerCysThrPheAlaGlnSerValSerSerAlaTyrThrIleAlaValVa 192
                                                                                                                                                                                             TOGTGCCAAACTTTTTTGTTGGATCACTACAGTATGACCCCAGGATTTTT 540
                                                                                                                                                                                                                                                     alLeuProAsnLeuArgAlaGlyThrLeuGlnTyrAspProArgIleTyr 175
                                                                                                                                                                                                                                                                                                                                                                                sAsnSerLeuCysTyrValLeuLeuIleTrpLeuLeuThrLeuAlaAlaV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTGCTACATCTGCCACAGCCTGAGATATGACAAGCITTAIAATCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrCysTyrIleCysHisSerLeuLysTyrAspLysLeuTyrSerSerLy 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGCGTTATTGGATGAGTGTTCAACATAAGAGAGCCATAGGJATGAACAGG
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                                                         Jackers R. Marulle S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allolo: Xenopus larvis: melatonin: receptor: untranslated region: PCR; meNA: half-lite: skin: amplification: primer; polymerase chain reaction: transmembrane domain, cellular signalling, inhibition, adenyiyl cyclase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xemopus melatonin receptor MEL-lAa long form coding sequence
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                                                                                                                  (ADIR ) ADIR & CIE.
                                                                                                                                                                              24 JIII.-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xomopus laevis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 leTleValSerLeuCysThrAlaArgValPhePheValAspSerSerAsn 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 LeuPheValAlaSerTyrTyrMetAlaTyrFheAsuSerCysLeuAsuAl
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                                                                                                                                                                                                                                          74 JHL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myddlation: intracellular, cyclic GMP, inhibitor, phosphodiesterase, ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 nAsc 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOV - 1 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACTGATGTCCTTATTGACTCCAAGACTGTTGTTTCTTGACACATCTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                     /product- MEL-lAs receptor protein
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alignment_scores:
                                                                                                                               amino acids shorter than those described in the prior art. Also the last 2 C-terminal amino arids encoded by those separates are different from the previously known proteins. This sequence is a long form of the novel receptor MEL-IAG also known as Mel 1-c(alpha). As compared to the short form (779064), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affort the half-life of the mRNA. The nucleotide sequence was isolated from cDNA derived from xenepus skin RNA and amplified using the primers 77967-76. The nucleotide sequence electedes a protein which is a 7 transmembrane receptor involved in celiular signalling. MEL-IAG has been shown to inhibit adenylyi cyclase, but both proteins can modulate intracellular phosphodiesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences 179063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MRL-IA. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. Also the la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (aut)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 25 26; 62pp; French.
                                                                              Sequence 1311 BP: 360 A: 250 C: 260 G: 414 T: 0 other:
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alignment_block: US-09-226-046-12 x T79063 Quality: 1244.00 Patic: 4.290 Percent Similarity: 91.195 Align seq 1/1 to: T/9063 from: 1 195 191 AGAATGCTGGAAATCTCTTTGTTGTTGTTTATTGGCTGATCTGGTT 240 159 alLeuProAsnLeuArgAlaGlyThrLeuGlnTyrAspProArglleTyr 175 141 UCISGGCAAIAFAITGGTCAITTTGTGTGTGTGAGGAACAAGAAGCTGC 190 16 terlAladerAlater.AlatysValteuffelbeibzileValValAspil 42 92 yTrpAsnLeuGlyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyL 109 76 ValAlaIleTyrFreTyrPreLeuValLeuMetSetIlePheAsuAsuGl 92 59 rqAsnAlaGlyAsnIlePheValValSerLeuAlaValAlaAspLeuVal 75 42 eLeuGlyAsnLeuLeuValIleLeuSerValTyrArqAsnLysLysLeuA 59 AAGCATGTGGTGGTTGGGTTGACATGGATACTATATTGCAA sAsnSerLeuCysTyrValLeuLeuIleTrpLeuLeuThrLeuAlaAlaV 159 TCAGUGTTATTGGATGAGTCTTGAACATAAGAGAGCGATAGCTATGAAGAGG 390 euSerValIleGlySerTlePheAsnIleThrGlyIleAlaIleAsnArg 125 REPROPERSIGNATION AND REPRESENTATION AND ARCHARD STREET TATTGCIACATOLOGGAGAGATATGAGAAAGTTTATAATCAAAG TyrdysTyrTledysHisSerLeuLysTyrAspLysLeuTyrSerSerLy 142 Percent Identity: 70.440 to: 1311 440

TOGTGOCAAACTTITTTGTTGGATCACTACAGTATGACCCCAGGATTTTT

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seq_documentation_block:
ID T09947 standard; cDNA; 1320
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77 - TUN- 1995 -
                                                                                                                                                                                                                                                                                                                                Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                         antibody: transgenic animal; drug screening; ds
                                                                                                                                                                                                                                                                                                                                                                                                                   melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder, jet-lag, day-night cycle disorder, culation; reproductive cycle; animal brooding; puberty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melatonin receptor; G-protein compled receptor, melanophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High-affinity melatonin receptor gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspValAlaAspArgValLysTrpLysProSerProLeuMetThrAsnAs 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all-fleTyrGlyLeuLeuAsnGlnAsnPheArgLysGluTyrArgArgI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTTTGTTTTAAGCTATTTCATGGCCTATTTTAACAGTTGTCTCAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTGATGTCCTTATTGACTCCAAGACTGTTGTTTCTTGACACATCTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
95W0-0807360
                                                                                                                                                                                                    32..1294
/*tag= 8
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                           /product= High-affinity melatonin receptor
                                                                                                                                                                                                       D
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: T09947 from: 1 to: 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor-agonists or receptor antagonists. Agonists may be used in therapy of circadian rhythm discreders such as jet-lag or day-night cycle disorders, to control ovallation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consensus sequence for initiation of translation. The Xenopus sequence has been used for isolation of homologous sheep, mouse and human melatonin receptor sequences. Receptor fragments which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laevis. The receptor is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins). The cDNA has been cloned from Xenopus dermal melanophores, and expressed in Escherichia coli Flanking ENA sequences of the 1st 2 Met codons both display a Korak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENA encoding high affinity melatonin receptor one – used to identify receptor agonists or antagonists e g for regulating circadian rhythm disorders or reproductive cycles
                                                                                            372 ICAGCGTTATTGGATCAGTCTTCAAGATAACAGCCATAGCTATCAACAGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO TO THE TITLE THE TITLE TO THE TITLE TO THE TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 COTGGSCATATATTSGTCATTTSGTCTGTCTGAGGAACAAGAAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1320 BF; 364 A; 278 C, 299 G, 379 T, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal for use as a model system to screen agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Fig 1; 115pp; English.
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17-JUN-1994;
lib TyrCysTyrileCysHisSerieuLysTyrAspiysLouTyrSerserTy 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CTCACCTCTGCCCTGGCGGTGGTTGTTATATTCACCATTGTTGTTGAGATGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interact with melatonin, or specific antibodies, may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence encodes a high-affinity melatonin receptor from Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 eLeuGlyAsnLeuLeuValIleLeuSerValTyrArgAsnLysLysLeuA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 LeuAlaScrAlaLcuAlaCysValLcuIlePheThrIleValValAspIl 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 ValAlaIleTyrProTyrProLeuValLeuMetSerIlePheAsnAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 rgAsnAlaGlyAsnIlePheValValSerLeuAlaValAlaAspLcuVal 75
                                                                                                                                                                                                                                                                      AMOGROGOTMOGRAATATOCATTOTOAGAMOAGTGGCYMTGTGAGGGGAC 371
                                                                                                                                                                                                                                                                                                                                                     yTrpAsnLeuGlyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGCTGTGTATCCCTATCCGGTCATTCTCATAGCTATTTTCCAGAATGG
                                                                                                                                                                          euSerVallleGlySerilePheAsnileThrGlyIleAlalleAsnArg 125
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                                                                                                                                                                                                                 Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR; mPNA; half-life, skin, amplification, primer, polymerase chain reaction, transmembrane demain: cellular signalling, inhibition; adenylyl cyclase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 AAGCAAAAGTTGACAAAACAGACTTGAGAAATTTCTTGACCATGTTTGT 771
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                           sAsnSerLeuCysTyrValLeuLeuIleTrpLeuLeuThrLeuAlaAlaV 159
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: T79066 from: 1 to: 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-226-046-12 x T70066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                b amino acids. The nucleotide sequence was isolated from cUNA derived from Xencpis skin PNA and amplified using the primers T79667-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-1Ab has been shown to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acids shorter than those described in the prior art. This sequence is a short form of the novel receptor MEL-lab shown as Mel 1-c(beta). As compared to the short form (T79066), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The MEL-lab sequences also differ from known MEL-lab teachers 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1147 BP; 313 A; 245 C; 240 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1, Page 33-34, 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-FEB-1997
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                                                                                                                                                   191 AGAAUGCIEGAAAFCIGITTEGTGAGTAGTGAGTATTAGAGATCTEGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-1A. The sequences encode proteins which are 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding functional metatonin receptor of Xenopus for screening for potential (ant)agenists useful for e g. treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-132635/12
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                                                                                                                                                                                                                                        141 CCTGGGCAATATATTGGTCATTTTGTCTGTCTGAGGAACAAGAAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibit adenylyl cyclase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike MEL-lAa (T79063) cannot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W25927
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                                                                                                    76 ValAlaTleTyrProTyrProLeuValLeuMc+ScrTlePhoAsnAsnGl 92
                                                                                                                                                                                                                                                                     42 eLeuGlyAsnLeuLeuVallleLeuSerValTyrArgAsnLysLysLeuA 59
                                                                                                                                                                                                                                                                                                                        92 yTrpAsnLeuGlyTyrLeuHisdysGlnValSerGlyFheLeuMetGlyL
                                                                GETGGT CTGTATCCCTACCCCACACCCCTATTAGCTATTTTGAAAAAA
                                                                                                                                                                                             rgAsnAlaGlyAsnIlePheValValSerLeuAlaValAlaAspLeuVal 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1240.00
Ratio: 4.276
milarity: 91.195
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/product= melatonin receptor MEL-lab
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Strosberg AD:
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seq_name: / 'Anala' Aradata genesesy genesean/NALMATIONT ITMEST
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Xemopus melatonin receptual MEI Jak long form ording weguter-
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                                                                                                                                                                                                          T79065 standard; cDNA to mRNA; 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      991
                                                                 10-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  nAsn 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEAGGAACTGAGGGAITGAAAAGTAAGCCTTCGCCAGCTGTAACCAACAA 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGCGTTATTGGATCAGTCTTCAACATAACAGCCATAGCTATCAACAGG
                                                                                                                                                                                                                                                                                                                                                                                CAAI 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allelleTyrGlyLeuLeuAsnGlnAsnFheArgLysGluTyrArgArg1 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euAlaValAlaSerAspProAlaSerMetValProArgIleProGluTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lValPheValLeuPheAlaIleCysTrpAlaFroLouAsnPhcIlcGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCAAAAGTTGACACCAACAGACTTGAGAAATTTCTTGACCATGTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysProLysLeuLysProGlnAspPheArgAsnPheValThrMetPheVa 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATATGGGTTTTAGTGATCCAAGTCAAACACAGAGTTAGACAAGACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCACCTGGTTCTACCTTGGCCTGACATGGATACTAACCATAATTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTGCTACATCTGCCACACCCTGAGATATGACAAGCTTTTTTAATCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyroysTyrIleCysHisSerLeuLysTyrAspLysLeuTyrSerSerLy 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euSerVallleGlySerIlePhcAsnIlcThrSlyIleAlaIleAsnAry 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGAGGCTTGGAAATATCCATTGTCAGATCAGTGGCTTCCTGATGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspValAlaAspArgValLysTrpLysProSerProLeuMetThrAsnAs 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTGATGTCCTTATGGACTCCAAGACTGTTGTTTTTTTGACACATCTAGA 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lelleValSerLeuCysThrAlaArgValPhePheValAspSerSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCATCTACGGTCTGCTAAATCAAAACTTCCGCAAGGAATACAAACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGITIGIGITAAGCIATIICATGGCCIATIITAACAGCIGICICAAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuFheValAlaSerTyrTyrMetAlaTyrPheAsnSerCysLeuAsnAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585
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aliqnment_block:
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                                                                                                                                                                                                                                     Align seg 1/1 to: T79065
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                                                                                                                                                                                                                                                                                                                                        Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melutionin receptor MEL-IA. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. This sequence is a long form of the novel receptor MEL-IAb also known as Mel 1-c(beta). As compared to the short form (T79066), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The MEL-IAb sequences also differ from known MEL-IA receptor sequences by 6 amino acids. The nucleotide sequence was isolated from cDNA derived from xenopus skin RNA and amplified using the primers 179967-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-IAb has been shown to modulate intracellular cOMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodioscorase, but unlike MEL-IAb (T70063) cannor inhibit adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allele, Xenopus laevis, melatonin, receptor, untranslated region, POR, mRNA, half-life; skin; amplification; primer, polymerase chain reaction; transmembrane domain, collular signalling, inhibition; ademylyl gyplase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fage 30-31; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. freating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis
191 AGAATGCTGGAAATCTCTTTGTTGTCAGTTTGTCTATTGCCGATCTGGTT
                                                                           141 CCTGGGCAATATATTGGTCATTTTGTCTGTCCTGAGGAAGAAGAAGCTGC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1312 BP; 365 A; 271 C; 267 G; 409 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jockers R, Marullo S,
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                                                                                                                                                     42 eLeuGlyAsnLeuLeuVallleLeuSerValTyrArqAsnLysLysLeuA 59
                                   rgAsnAlaGlyAsnIlePheValValSerLeuAlaValAlaAspLeuVal 75
                                                                                                                                                                                                                                                                                                                                        Quality: 1240.00
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/product= melatonin
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Sord_names (1997) ____ for this to provide Controls the NAME CAT TOWNS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24: GTTGCTGTGTATCCCTATCCGGTAATTCTCATAGCTATTTTCCAGAATGG
                                                                                                                                          34.2 nAsn 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCAAAAGTTGACACCCAACAGAACTTGAGAAAATTTCTTGACCATGTTTGT
                                                                      CAAT 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuPheValAlaSerTyrTyrMetAlaTyrFheAssSertSysLeuAssAl 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GANTATOGGTTTTAGTGATGTAAGTGAAATGAGAGAGTTAGAGAGTTG 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTAGTGCALLITALAGTGCGCTCITAGTGTGAGAGATIGTGGCTAGTTAA 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTOTOCCAAACTTTTTTGTTGGATGACTACAGTATGACCCCAGGATTTIC 540
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                                                                                                                                                                                                         GGAGGAACTGAGGGATTGAAAAGTAAGTCTTCGCCAGCTGTAACCAACAA 1540
                                                                                                                                                                                                                                                                             AspValAlaAspArgValLysTrpLysPruSerPreLegMetThrAsnAs 342
                                                                                                                                                                                                                                                                                                                                                TATTGATGTCCTTATGGACTCCAAGACIGITGTTTGTTTGACAGAFGTAGA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCATCTACGGICIGCIAAAICAAAACTTCCGCAAGGAAIACAAACGAA
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Reppert SM

(MASS-) MASSACHUSEITS GEN HOSPITAL.

95WO-USO7360 95US-0319887 94US-0261857 94US-0319887

P-PSDH: R88414

WPI: 1995-858706

Claim 10; Fig 6; 115pp; English

TNA PER diag high affinity melatinic temptor menor meed to identity receptor agonists or antagonists eng. for regulating circadian

disorders or reproductive cycles

06-JUN-1995; 17-JUN-1994; 07-OCT-1994;

07-JUN-1995;

28-DEC-1995

W09535320-A1

/product= High-affinity melatonin-lb receptor

Location/Qualifiers 13..1098

/*tag= a

Homo sapiens

melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disordar; jet-lag: day-night cycle disorder; ovulation, reproductive cycle, animal breeding, puberty; antibody; transgenic animal; drug screening; ds.

High-affinity melatonin-1b receptor gene.

Melatonin 15 receptor, human;

a protein-coupled receptor

16-AUG-1996

(first entry)

Spill Landings

FF TRE A

303 G. 251 T: 0 other:

The sequence encodes human high-affinity melatonin-lb receptor. CC which is a membrane protein, coupled to quanine nucleotide binding CC proteins (G-proteins), and has been closed by PCF amplification of thuman genomic DNA, using primers based on the 3rd and 6th CC human genomic DNA, using primers based on the 3rd and 6th CC recepting of a human brain cDNA library. The genomic sequence has comening of a human brain cDNA library. The genomic sequence has come interested about 19 km in the 1st cytoplasmic loop region.

CC Intron PCR with primers T09953-54 and 43 human-rodent somatic conclusion.

CC charmsone 11221 22 Filmers T09951 [classifier the human MNTRIB denote to charmsone 11421 22 Filmers T09951 [classifier protein framents which consists and 11221 22 Filmers T09951 [classifier and protein seed as contract with melatonin, or specific and protein say be used in the tast with melatonin, or specific and protein say be used in the paper of citradian rhythm disorders such as jet-lag or day high control countries and hardonists may be used in the paper of control control countries and animals.

CC The receptor generated he in seasonally broading animals Animans.

CC The receptor generated also be expressed in a transactic animal for use as a model system to several agonists and antagonists.

seq_documentation_block:
fb Tem952 standard; cDNA; flo5 BP

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Align seg 1/1
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                                                                                                                                                                                                                                                                                       253 ProLeuAsnPheIleGlyLeuAlaValAlaSerAspProAlaSerMetVa 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508 AGTACACGGCGGCAGTGGTGGTCATCCACTTCCTCCTCCCTATCGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558 GIACGACCCACGCATCIATICCTGCACCITCATCCAGACCGCCAGCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 TGGCCATCTTCTATGACGGCTGGGGGCTGGGGGGAGCAGCACTGCAAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 pGiyAlaArqProSerTrpLeuAlaSerAlaLeuAlaCysValLeuIleP 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heAsnSerCysLeuAsnAlaIleIleTyrGlyLeuLeuAsnGlnAsnPhe 302
                                                                                                                                 lproArgIleProGluTrpLouPheValAlaSerTyrTyrMetAlaTyrF 286
                                                                                                                                                                                                                  CCACTTAACTGCATCGGCCTCGCTGTGGCCATCAACCCCCCAAGAAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                snPheValThrMctPheValValFheValLeuPheAlaIleCysTrpAla 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laTyrThrIleAlaValValPheHisPheLeuValProMetIleIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CICCICACCGIGGIGGCCITGCTGCCCAACTTCTTTGTGGGGICCCIGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spLysLeuTyrSerSerLysAsnSerLeuCysTyrValLeuLeuIleTrp 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAlaValAlaAspLeuValValAlaIleTyrFroTyrFroLeuValLeuM 86
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                                                                        TOPOPAGATORITAAGAGATAITTGTPAGTAGTAGTTAGTGGGTTATT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAAAGCCAASCCAGAGAGAGGCIGIGIGIAAGCCCAGCGAGIIGGGGA 757
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seq_documentation_block:
TD Z25518 standard: cDNA: 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physiologically active peptide; receptor binding galanin receptor; GALR1; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function, appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
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                                                                                                                                                                                                                                                                                                       The present invention describes poptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides binding to galanin receptor proteins, used to kidney functioning \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WFI, 1999-572170/48.
P-PSDB; Y45129.
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21-SEP-1998;
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Sequence 1041 BF; 211 A,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fage 125-126; 153pp; Japanese.
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98JP-0266972
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   329 0;
255 G; 245 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kitada
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alignment_block:

Percent Similarity:

alignment_scores

Quality: Ratio:

340.00 1.726 60.061

vaps: 11 Percent Identity: 29.258

50.55

225-045-12 x Z25518

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Align seq 1/1 to: 225518 from: 1 to: 1041
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                                                                                                                                                         253 oLeuAsnPheIleGlyLeu......AlaValAlaSerAspP
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25% roAlaSerMetValProArgIleProGluTrpLeuPheValAlaSerTyr 281
                                                                                   740 CCATCATGTCATCCAGCTCTGGGGTGAGTTCGGAGGATTGCCGGTGAGCC 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 rqValLysProAspArqLysProLysLeuLysProGlnAspPheArgAsn 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               642 CTGC!!!!GC!A!GCGAAGG!!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 ATCACOSTOCTOGOGOGOGAGCAAACCGGGGCAAGCGGGGGGGGGGACGACGAA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14/ TyrValLeuLeuLleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLe 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 GAGCATOTTCACCCIGGCGGGGATGTCTGTGGAIGGCTAIGIGGCGATIG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO GCCTTCATCTGCAAGTTTATACACTACTTCTTCACCGTGTCCATGCTCGT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 CCFCFTCAFOCFCAACCFCACCAFCCCAGACCFGCCCTACCFGCTGTTGT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       se nilebhevalvalserieuAlavalAlaAspteuvalvalAlaileTyrp 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 HeLeuSerValTyrArqAsnLys.....LysLeuArqAsnAlaGlyAs 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1' qGlyAspGlyAlaArqProSerTrpLeuAlaSerAlaLeuAlaCysValL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *O roTyrFroiesValbeuMetSerIleHheAsnAsnGlyIrpAssLeuGly 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 oullePhoThrIleVal.....ValAspIleLeuGlyAsnLeuLeuVal 48
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                                                                                                                                                                                                                                                                                                                                Phe ValThr \texttt{MetPheValValPheValLeuPheAlaIleCysTrpAlaPr}
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                                                                                         alignment_scores:
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                alignment_block:
US-09-226-045-12 x 297204
                                         Percent Similarity:
                                                                                                                                                                              calininergic receptors are useful as biological and pharmocological research tools and for production of antibodies. Agonists of such receptors are useful as analysesies. Probes directed against the usens are useful for detecting expression of galaninergic receptors. It detecting expression of galaninergic receptors. It detecting expensions, for diagnosping neurological, endiowascular, endocrine or psychiatric disorders and for defecting and isolating nucleic acid sequences coding for galaninergic
                                                                                                                                                                                                                                                                                                                                  New galanin receptor gene - useful for diagnosing neurological cardiovascular, endocrine or psychiatric disorders.
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1393 TGCACCTTCGTCTTCGGCTACCTGCTGCTCCTGCTCTCTCATCTTCTG 1442
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                                                                                                                        1581 CATCCATCTCTGGGCTGAGTTTGGAGTTTCCCGCTGAGGCCGGCTTCCT 1630
                                                                                                                                                                                                                                                       1531 СТІСТСЯТАСТСЕТТСІСТСТТІССАЛІТІТСІВСЕТСЕСССАССАСТ 1580
                                                                                                                                                                                                                                                                                                                                                                                      1483 ... AACATGTCAAAGAAGTCTGAAGCATCCAAGAAAAAGACTGCACAGACA 1530
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                                                268 ctValProArgIleProGluTrpLeuPheValAlaSerTyrTyrMetAla 284
                                                                                                                                                                                             256 eIleGlyLeu.
                                                                                                                                                                                                                                                                                                                  240 MetPheValValPheValLeuPheAlaIleCysTrpAlaProLeuAsnPh 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 nLeuArqAlaGlyThrLeuGlnTyrAspProArqIleTyrSerCysThrP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 eGlySerIlePheAsnIleThrGlyIleAlaIleAsnArgTyrCysTyrI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 sTyrLeuArgIleTrpIleLeuValLeuGlnValArgGlnArgValLysF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 leCysHisSerLeuLysTyrAspLysLeuTyrSerSerLysAsnSerLeu 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 GlyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerValIl 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 yrProTyrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 alLeuIlePheThrIleVal.....ValAspIleLeuGlyAsnLeuLeu 47
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                                                                                                                                                                                      AlaValAlaSerAspProAlaSerM 268
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..ACCGCCCACTGCCTGGCG 1662

- 1563 TACAGCAATTCCTCCGTGAATCCTATCATTTATGCATTTCTCTCTGTAAAA 1712 285 TyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeuLeuAsnGlnAs 301
- 1713 TITCAGGAAGGCCTATAAACAAGTG 1737 301 nPheArgLysGluTyrArgArgIle 309

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About: Results were produced by the GenCore software, version 4.5,\, ropyright (a) 1993-2000 computen Ltd.
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Query: US-09-226-046-12
Query length: 350_
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Database length: 80580151
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-MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model -MODEL-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-frame-Lp2.model-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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STREET: 2:
                                 COUNTRY:
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/con2_6/ptodata/2/ina/5A_COMB.sec; US-08-417-103-15 + 303.00 605.85 / con2_6/ptodata/2/ina/5A_COMB.sec; US-08-417-103-15 + 303.00 605.85 / con2_6/ptodata/2/ina/5A_COMB.sec; US-08-417-103-5 - 203.00 603.47 con2_6/ptodata/2/ina/5A_COMB.sec; US-08-147-103-5 - 203.00 603.47 con2_6/ptodata/2/ina/5A_COMB.sec; US-08-147-592A-3 - 203.00 603.48 / cgn2_6/ptodata/2/ina/5A_COMB.sec; US-08-147-592A-3 - 203.00 605.48 / cgn2_6/ptodata/2/ina/5A_COMB.sec; US-08-147-592A-3
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                                                                                                                                                                                  Partient Similarity: 100,000
Alian sed 1/1 to 08-08-466-109A-11 (rod)
                                                                              79-94-22+-046-12 x US-08-466-103A-11
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INPOPMATION FOR SEQ ID NO.
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APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION: FECEPTOPS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-0CT-1994
PRIOK APPLICATION DATA.
APPLICATION UMBER: 08/26
FILING DATE: 17-JUN-1994
ATTOPNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTECULE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Flaser, Jamis K. PEGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/319,887 FILING DATE: 07-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence Location: 33, 1082
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                                                                                                                                                                                                                                                                                          Quality: 1815.00
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                                                                                                                                                                        284 laTyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeuLeuAsnGln 300
                                                                                                                                                                                                                                     833 CATGOTOCCIAGGATOCCAGAGIOGCTGTTTGTGGCCAGTTACTAGATGC 882
                                                                                                                                                                                                                                                                                                                                                      784 TGGGCTCTCTGAACTTCATTGGCCTGGCCTGTGGCCTCTGACCCCGCCAG 832
                                                                                                                                                                                                                                                                                                                                                                                                             25.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 COMMANAGAGGGGGAAACCTGACCGGAAACCGAAACTGAAACCAGAGGACT 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 erserAlaTyrThrIleAiaValValValPheHisPheLeuValProMet 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 rLouGlnTyrAspProArgIleTyrSerCysThrPboAlaGlnSorValS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1': 110*TrpteuteuteuthrteuAlaAlaValteuProAsnteuArgAlaGlyTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 CATCACCOGCATCGCCATCAACCGCTACTGCTACATCTGCCACAGTCTCA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 oileThrGlytleAlatleAssArqTyrCysTyrTleCysHisSerLeuL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 CAAGTOAGTGGGTTCCTGATGGGCCTGAGCGTCATCGGCTCCATATTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 TCAICTICACCATCGTGGTGGACAICCTGGGCAACCTCCTGGTCATCCTG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R4 alleuMetSerllePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisCys 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rMetValProArgIleProGluTrpLeuPheValAlaSerTyrTyrMetA 284
                                                                                                                                                                                                                                                                                                                                                                                                             TrpAlaProLeuAsnFheileGlyLeuAlaValAlaSerAspFroAlaSe 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lArgClnArgValLysProAspArgLysProLysLeuLysProGlnAspF 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOTOCAGIACIANTOGIANISATOTACTOGTNICACOTTOGGOCAGTOGGTCA 582
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Syspector 1 Application US 09280420 Patent No. 6037131 GENERAL INFORMATION:
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                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                    Quality: 1570.50
Ratio: 4.688
Percent Similarity: 44 401
                                                                                   Align seg 1/1
                                                                                                                                                                  US-04-226-046-12 x US-04-280-420-1
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INFORMALION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2772 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NAMES US CONTROL NAME ( FASTISSE FOR WINDOWS VOISION AFFILIATION NAMES US OF THE CONTROL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1033 AACCGTCTCCACTGATGACCAACAATAATGTAGTAAAGGTGGACTCCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 18-JUL-1996
ATTOFNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reppert, Steven M. (1716 of INVENTION: MELATONIN TITLE OF INVENTION: PEGULATOR NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 qValPhePheValAspSerSerAsnAspValAlaAspArqValLysTrpL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00
SELECTION INFORMATION:
TELEPHONE: 617/542-890
TELEFAX: 617/542-890
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1 MetGlnGlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeu.. 16
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LCCATION: 1270...2328
OTHER INECEMATION: introdecoding sequence between positions 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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STFANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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225 Franklin Street
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REGULATORY REGIONS AND USE:
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1270 ΑΤΟΛΑΘΊΘΙΑΤΘΤΟΑΘΟΘΑΘΟΤΘΟΙΟΑΑΤΘΟΓΑΘΤΑΘΟΑΘΟΛΟΓΟΚΑΘ

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1420 GTCATCCTGTGTGTGTATACGGCAACAACAACATCAGGAACTCAGGGAATAT 1469
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2170 CTGAATCAGAATTTCAGAAAGGAAAGAAAAAAAAAGATTATTGTCTCGTTGTG 2219
                                                                                                                  2120 ACTACCTOSPOTANCIO INTERNATIONALI MARIO DANTACTATOSCACTA 2160
                                                                                                                                                                                                                                                                                                                                                          2020 SCCATTTGTTGGGGCCCCACTCAACCTCATAGGTCTTATTGTGGCCTCAGA 2069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 rIlePheAsnIleThrGlyIleAlaIleAsnArgTyrCysTyrIleCysH 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 | LeuGlnValArqGlnArqValLysProAspArgLysProLysLeuLysP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 roGlnAspPheArqAsnPheValThrMetPheValValPheValLeuPhe 247
                                                                                                                                                                     281 yrTyrMetAlaTyrPheAsnSerCysLeuAsnAlaileIleTyrGlyLeu 297
                                                                                                                                                                                                                                 248 AlaIleCysTrpAlaProLeuAsnPheIleClyLeuAlaValAlaSerAs 264
                                                  298 LeuAsnGlnAsnPheArgLysGluTyrArgArgIleIleValSerLeuCy 314
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seq_documentation_block:
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                                                                                                                                                                NAME/KEY: Coding Sequence LOCATION: 1...1059
LOCATION: 1...1059
OTHER INFORMATION:
US-(8-466-103A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08466103A Patent No. 5856124 GENERAL INFORMATION:
alignment_block:
US-09-225-046-12 x US-08-466-103A-13
                                                                                                        alignment_scores:
                                                   Ratio: 4.6%2 percent Similarity: 94.334
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION POP SEQ ID NO: 13.
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PPLOF APPLICATION DATA:
APPLICATION NUMBER: 08/261.857
FILING DATE: 17-JUN-1994
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: li
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                                                                                         Quality: 1552.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,819
                                                       Percent Identity: 83.286
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                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMKEP: 08/2*
FILING DATE: 17-JUN-1994
ATTOPNEY/AGENT INFOPMATION:
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER FILING DATE: 06-JUN-1 CLASSIFICATION. 435
PPTOP APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reppert, Steven M. APPLICANT: Ebisawa, Takashi
                                                               FEATURE:
                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HIGH-AFFINITY MELATONIN TITLE OF INVENTION: PECEPTORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 AspSerVal 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      951 САСАФОСААФАТОТТСТТТОТФЗАВАВТТОАААТБААФААФААСАФАТААФА 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 sThrAlaArgValPhePheValAspSerSerAsnAspValAlaAspArgV 331
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                                                                                                                                                 TYPE: n
LUCATION: 49...11 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                               NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819 REFERENCE, DOWNET NUMBER: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/3 FILING DATE: 07-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIF: 02110-2804
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STREET: 2:
                                       NAME/KEY: Coding Sequence
                                                                                                        TOPOLOGY.
                                                                                                                         STRANDEDNESS:
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o. 5856124
                                                                                                                                             н: 1149 base pairs
nucleic acid
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                                                                                                        linear
                                                                                                                                                                                                                                                      617/542-5070
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                                                                                  DNA (genomic)
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                                                                                                                            double
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alignment_block:
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Ratio: 4.553
Fercent Similarity: 94.051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-126-046-12 Y MS-OB 466-103A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 COTOCATOCTCATOTTCACCATOCTGGTGGACATOGTGGGCAACCTCCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 ACCCCTTGGCGCTGGCGTCTATAGTTAACAATGGGTGGAGCCTGAGCTCC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 GITIGIGGIGAGGGIGGCAGTTGCAGACCTGCTGGTGGCGGTGTATCCGT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 GIGGTCCTGTCCGTGTATCGGAACAACAAGCTGAGGAACGCAGCGAATGT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 ANGGUCANCESCASCASCASCASCACTÓCIONACCTOTÓCAGGCCGCGCGCCCGG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 GGTTTTCAGNATCAGGGGAATTGCCATGAAGGGGTATTGCTGCATCTGCC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 rilePheAsnileThrGlyIleAlaileAsnArgTyrCysTyrIleCysH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 laCysValLeuIlePheThrIleValValAspIleLeuGlyAsnLeuLeu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 .ArgGlyAspGlyAla.....ArgProSerTrpLeuAlaSerAlaLeuA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 GTGTTCCTGATCTGSACGCTGACGCTGGTGGGGGATGGTGGCGGAACCTGTG 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 ValLeuLeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuAr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 ePhevalvalSerLeuAlaValAlaAspLeuValValAlaIleTyrProT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 ValileLeuSerValTyrArgAsnLysLysLeuArgAsnAlaGlyAsnIl 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 gAlaGlyThrLeuGlnTyrAspProArgIleTyrSerCysThrPheAlaG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 yrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyr 97
                                                                                                                                                                                                                                                                             688 GTTCCGATGCTGGTAGTCGTCTTCTGTTAGCTGAGAATCTGGGGCCCTGGT 737
                                                                                                                                                                                                                                                                                                           198 ValproMetIleIleValllePheCysTyrLeuArglleTrpIleLeuVa 214
                                                                                                                                                                                                                                                                                                                                                                             6.8 AGTOCGTCAGCTCAGCCTACACGATCGCGTGGTGGTGGTGTTCCATTTCATA 687
                                                                                                                                                                                                                                                                                                                                                                                                                      181 lnSerValSerSerAlaTyrThrIleAlaValValValPheHisPheLeu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 LeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerValIleGlySe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 roGlnAspPheArqAsnPheValThrMetPheValValPheValLeuPhe 247
                                                                                                                                                                                    738 TOTTCAGGTCAGATGGAAAGGGAAAGGGAAACTGAAGC 787
                                                                                                                                                                                                                               214 | LeuGlnValArqGlnArqValLysProAspArgLysProLysLeuLysP 231
                                      248 AlaileCysTrpAlaProLeuAsnPheIleGlyLeuAlaValAlaSerAs 264
                                                                                        788 COUNSEACTICAGSANTÉTTOTÓACCATÓTTTGTGGTTTTTGTGCTCTTI 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isSerLeuLysTyrAspLysLeuTyrSerSerLysAsnSerLeuCysTyr 147
percent Identity: 81.303
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seq_name: /ngn2_6/ptodata/2/ina/mp_nnm.seq_us-nm-466-103A-5
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 5, Application US/08466103A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1088 TTAAACGCAAACCCTCTCCATTAATAGCCAAACCATAACCTAATAAAGGTG 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 YrTyrMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeu 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 pProAlaSerMetValProArgIleProGluTrpLeuPheValAlaSerT 281
                                                                                                                            TELEFAX: 617/542-8906
INFORMATION, FOE SED IN NO.
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HIGH-AFFINITY MELATONIN TITLE OF INVENTION: RECEPTORS AND USES THEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2\cdot 0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM.
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/2
AFFLICATION NUMBER: 18/2
FILING DATE: 17-JUN-1994
                                                                                                                                                                                                                                                                                  FILING DATE: 17-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                LENGTH: '867 base-pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                       TELEPHONE: 617/542-5070
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                      FEATURE:
                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUDRESSEE, FISH & LL. Street STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                           ASPLICATION NUMBER FILING DATE: 07-00
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                                                                                                                                                                                                                                               NAME: Fraser, Janus K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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NAME/KEY: Coding Sequence
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Ebisawa, Takashi
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                                        DNA (genomic)
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US-08-466-103A-5

OTHER INFORMATION

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aliqnment_block:
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Ratio: 5.119
Percent Similarity: 97.578
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                                                                 697 GOCCACITACITACATGCCGTAIIICAACAGCIGCCICAATGCCAITAIAI
                                                                                                                                                                                                       5-8 | OPOTECTOACOCCOCCAPATOSTOCCTAGGATOCCAGAGIGGCIGTITGI | 647
                                                                                                                                                                                                                                                                                                                                                 548 TOCTTTTTGCCATTTGCTGGGCTGCTGTGAACTTGATTGGGCTGGGCGTG 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 HebesValledShvalArqOharqValLysProAspArqLysProLy 228
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                                                                                                                                                                                                                                                                            252 AlasorAspFroAlaSorMotValFroArqIloEtcSluTrpLeuFheVa 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 ATCCTGGTTCTCCAGGTCAGACACAGAGGTGAAACCTGAGGGGAAACCGAA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COR ACTIOCICCOCCATGATCATAGICATCTTCTGTTACCTCAGAAATATGG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 isPheLeuValProMetIleIieValIlePheCysTyrLeuArqIleTrp 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TB rPheAlaGlnSerValserserAlaTyrThrIleAlaValValValPheH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHR ANCOTOCOTOCOGOACTOTOCACTACGAGGATOTACTOGIGOAC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 AsntouArgAlaGlyThrLouGlnTyrAspProArgIleTyrSerCysTh 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 TOGOTA ETTGCACTGCCAAG FCANTONISTER FORMA FORMANCITGAGINTO 150
                                                                                                                                                                                                                                                                                                                                                                                                                   245 altemPheAlaTleCysTrpAlaProLeuAsnPheTleGlyLeuAlaVal 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 SLeutysProGinAspPheArgAsnPheValThrMetPheValValPheV 245
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                                                                                                                                  lAlaserTyrTyrMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleT 295
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Percent Identity: 96.885
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alignment_scores:
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                     ouality: 1244.00
Ratio: 4.290
Percent Similarity: 91.195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEMERAL IMFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION: HIGH-ARFINITY MELATONIN
'IITLE OF INVENTION: PECEPTOPS AND USES THEREOF
NUMBER OF SECTENCES: 29
                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617/542-5070
TELEFAX: 617/542-8006
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEGISTRATION NIMBER: 34,819
PEFERENCE/PUDKET NUMBER: 007×5/250002
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 aAspArgValLysTrpLysProSorProLouMeUThrAsnAsnAsnValV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              848 TAAAGGTGGACTCCGTT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         748 LOSOTOGRIGAGAGOCAGGSTATIOTITIGIGGAGAGGTCTAAGGAGGTGGC 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 alLysValAspSerVal 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 SerLeuCysThrAlaArgValPhePheValAspSerSerAsnAspValAi 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                               NAME/KEY: Coding Sequence LEGATION: 32...1291
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K PEGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95 SOFTWARE: FastSEQ for Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                            1320 base pairs
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06-JUN-1995
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percent Identity: 70.440
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alignment_block
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 LenalaSerAlaLeuAlaCysValLoutleFheThrILoValValAspIl 42
|||::::||||||:::||||||:::
||22 CTOACCTCTGCCCTGGCGFFGFFCTTAFATTCACCATGTTGTGGATGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 AAGCAGGTGGTGGTTGGGGTGATATGGATACTAACTATAATTGCAA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 TyrCysTyrIleCysEisSerLeuLysTyrAspLysLeuTyrSerSerLy 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 TOAGOGITALIGGATOAGICITGAACATAACAGCCATAGCTATOAACAGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 euserVallleGlySerliePheAsnlleThrGlyIleAlalleAsnArg 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 AIGGAGGCTIGGAAATAIGCAITGTCAJATCAGTGGCTTGCTGATGGGAC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 GILGETGIGIATOOOTATOOGGIGATIOTOATAGGTATITTCCAGAATOG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 TOTTGCACATITGCSCAGACAGTGAGTTCCTCATACACCATACAGTAGT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522 TOGTGOCAAACTTTTTTGTTGGATCACTACAGTATGACCCCAGGATTTTT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 alLeuProAsnLeuArgAlaGlyThrLeuGlnTyrAspProArgIleTyr 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 sAsnSerLeuCysTyrValLeuLeuIleTrpLeuLeuThrLeuAlaAlaV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 TATTSCTACATCTSCCACAGCCTGAGATATGAGAAGCTTTATAATCAAAG 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 SerCysThrPheAlaGlnSerValSerSerAlaTyrThrIleAlaValVa 192
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922 TGITATATATGGTGCTAAATGAAAAGTTCCGCAAGGAGTACAAAAGAA 971
                                                               292 allelleTyrGlyLeuLcuAenGlnAsnPheArgLysGluTyrArgArgI 309
                                                                                                                                             872 CIGITISITITAAGCIATITCATGGCCTATTTTAACAGTTGTCTCAATGC 921
                                                                                                                                                                                                     276 LeuPheValAlaSerTyrTyrMctAlaTyrPheAsnSerCysLeuAsnAl 292
                                                                                                                                                                                                                                                                           822 TTGCTGTGGCCATTAATCCGTTTCATGTGGCACCAAAGATTCCAGAATGG 871
                                                                                                                                                                                                                                                                                                                                              259 euAlaValAlaSerAspProAlaSerMetValFroArgIleFroGluTrp 275
                                                                                                                                                                                                                                                                                                                                                                                                                         772 GGTCTTTGTACTTTTTGCAGTTTGCTGGGCCCCTTAAACTTTATCGGCC 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 LysProLysLeuLysproGlnAspPheArgAsnPheValThrMetPheVa 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 rgIleTrpIleLeuValLeuGlnValArgGlnArgValLysProAspArg 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 ValAlaIleTyrProTyrProLeuValLeuMetSerIlePheAsnAsnCl 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 eLeuGlyAsnLeuLeuVallleLeuSerValTyrArqAsnLysLysLeuA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 lValPheValLeuPheAlaIleCysTrpAlaProLeuAsnPheIleGlyL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ivaiPheHisPheLeuValProMetIleTleValIlePheCysTyrLeuA 209
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seq_name: /cgn2_6/ptodata/2/ina/5E_CCMP.seq-H8-H8-455-103A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                  alignment_block:
                                                                                                         alignment_scores:
                                                                                                                                                                      US-08-466-103A-15
                                                  Ratio: 3.886
Percent Similarity: 83.582
US-09-226-046-12 x US-08-466-103A-15
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                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 15:
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APPLICANT: EDISAWA, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: PRICEPTORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 nAsn 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319/887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                    MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPERENCE/INCRET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIF: 02110-2804
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                                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 13 .1098
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fraser, Janis R PEGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                             Quality: 1088.00
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                                                                                                                                                                                                                                                                                                                                             1105 base pairs
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617/542-8906
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                                                                                                                                                                                                                                                                                        linear
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                                                          Gaps: 1 Percent Identity: 61.194
                                                                                                 Length:
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Alium seq 1/1 to: @S-08-466-103A-15 from: 1 to: 1105
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                            286 heAsnSerCysLeuAsnAlallelieTyrGlyLeuLeuAsnGlnAsnPhe
                                                                                                                                                                                                                                     HIR CONCITANCIBUATORSCOTOSCIPATORSCOTATORASCOTORASANAMESSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 LouLouThrLouAlaAlaValLouProAsnLouArgAlaSlyThrLouGl loy
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                                                                                                                                                          259 | ProArgIleProCluIrpLeuPheValAlaSerTyrTyrMetAlaTyrP 286
                                                                                                                                                                                                                                                                                                      253 ProtenAsnPheIleGlyLeuAlaValAlaSerAspProAlaSerMetVa 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 SorGlyPhoLouMotGlyLouSerValIleGlySerIlePhoAsnIleTh 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 ....ccrcdaccrcccrsssrsscreeasesersreesesscscscrcarcs 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 TyrArqAsnLysLysLeuArqAsnAlaGlyAsnIlePheValValSerLe 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 heThrileValValAspileLeuGlyAmnLeuLeuValIleLeuSerVal 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 pClyAlaArgFroSerTrpLeuAlaSerAlaLeuAlaCysValLeuIleP 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANAGCCAAGCCAGAGAGAGATGTGTGTTGAAGGGTAGGGACTTGGGGGA 757
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seq_documentation_block:
    Sequence 47, Application US/OB513974B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER - PCI/TP
ETLING DATE: 10-AUG-1995
PRIOR APPLICATION NUMBER. JP 7-0
APPLICATION NUMBER. JP 7-0
ETLING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-0
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-3
FILING DATE: 28-DEC-1994
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TITLE OF INVENTION: PROTEIN, AND USE THERFOR NUMBER OF SEQUENCES: 380
CUPRESPONDENCE ACCRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
                                                                                                                                                      FILING DATE: 02-NOV-1994
PHICH APPLICATION DATA:
APPLICATION NUMBER: TP 6:
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Fluppy
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                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
                                                                                      APPLICATION NUMBER FILING DATE: 30-S
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 7-057186 FILING DATE: 16-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 14-SE
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alignment_block:
US-09+205-045-12 x US-08-513-9748-47
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PEEPPENTE/JOJUNET NUMBER 4575
PELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-440
TELEPAX 517-523-6440
INFORMATION FOR SEC ID NO 47
REDITENTS CONTROLLED NO 47
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APPLICATION NUMBER: JP 6-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                       407 COATTGTGCACTGGGGCACTCTGCTCCTCAGGGTGTCCCGCAACGCA 456
                                                                                                                                                                                 128 yrIleCysHisSerLeuLysTyrAspLysLeuTyrSerSerLysAsnSer 144
                                                                                                                                                                                                                                   357 GCTGGTGAGCATCTTCACCCTGGCCGCGATGTCTGTGGATCGCTACGTGG 406
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                                                                                                                                                                                                                                                                                                                                307 CIEGGCGCCTICATCIGCAAGTTTATACACTACTICITCACCGIGTCCAI 356
                                                                                                                                                                                                                                                                                                                                                                                                                          257 TOTTOTOCATOCCTTTTTCAGGGGAAGGGTGTATGGAGTGGGGGAGGTGGGGGG-308
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                                               145 LeuCysTyrValLeuLeuTleTrpLeuLeuThrLeuAlaAlaValLeuPr 161
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161 oAsnLeuArgAlaGlyThrLeuGlnTyrAspProArgIleTyrSerCysT 178
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11-AUG-1994
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seq_documentation_block:
    Sequence 341, Application US/Ud513974B
    Patent No. 6114139
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   859 GUCCATTGCCTGGCATACAGCAACTCCTCAGTGAACCCCATCATATATCC 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 erAspProAlaSerMetValProArgIleProGluTrpLeuPheValAla 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         777 GCTGCCCCATCATGTCGTCCACCTCTGGGCTGAGTTTGGAGGTTGGAGGTTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: G PROTEIN COUPLES RETEDITOR PROTEIN, TITLE OF INVENTION: PRODUCTION, AND USE THEREOF NUMBER OF SEQUENCES: 380 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        827 IGACGCCAGCTTCCTTCTTCAGAATC
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                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CUPRENT APPLICATION DATA:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA-
APPLICATION NUMBER:
FILING DATE: 10-ANG-
                                                                                                                                                                                                                                                                                                                       STREET:
                                                                    CLASSIFICATION:
                                                                                      APPLICATION NUMBER FILING DATE: 14-SE
                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                         Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohqi, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinuma, Shuji
                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujii, Ryo
Ohtaki, Tetsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hosoya, Masaki
    10-AUG-1995
                                                                                    14-SEP-1995
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alianment_block.
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Patio: 1.704
Percent Similarity: 58.788
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                                                                                                                                                                                                                                                                                                                                                                US-09 225-046-12 x US-08-513-974B-341
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: TP 7-007177
FILING DATE: 20 JAN-1995
F91OR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 29-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NECRMATION FOR SEQ ID NO: 341.
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: JF 6-236357

FILING DATE: 30-SEP-1555

PILING PART: 30-SEP-1555
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APPLICATION NUMBER: JP 7-
FILING DATE: 19-AUG-1995
PMICH APPLICATION NUMBER: JP 7-
APPLICATION NUMBER: JP 7-
                                               SHI COCTOCTACTOTTTCCCCTCATTTCCCCATACACACACTCCTCAGCAACAGA 636
                                                                                                                                                                                                                              SUM GAAGGGAATGGGAGGGAAC...GGAGAGGGGGGAGGGGGGAGTGGAGGGG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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SENCTH: 1607 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 6-189274
FILING INTE: 11-AUG-1994
FFIGR APPLICATION DATA:
APPLICATION NUMBER: 15-6-184273
FILING DATE: 11-AUG-1945
FFIGR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-SEP.
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                                                                                                                                         5% GOTOTTCGGCATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPIOR APPLICATION DATA:
47 LeuValileLeuSerValTyrArgAsnLys.....LysLeuArgAsnAl 61
                                                                                                                                                                                                                                                                      2 GludlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeuArg., 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: 008
LOCATION: 481..1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 6-189272 FILING DATE: 11-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME:
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                                                                                       ysValleuIlePheThrIleVal.....ValAspIleLeuGlyAsnLeu 46
                                                                                                                                                                            ......GlyAspGlyAlaArqProSerTrpLeuAlaSerAlaLeuAlaC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Resnick, David S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Percent Identity: 27 879
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seq_name: [^pgn2_6/ptn3ara/2/ina/6_00MH seq.05-08-08-08-108-1
                                                                                                                                                                                  1339 GCCCATTGCCTGGCATACAGCAACTCCTCAGTGAACCCCCATCATATATGC 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1207 AAGACTGCACAGACCSTCCTGGIGGTCGITGIAGIAIIIGGCATAICCIG 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 elleValllepheCysTyrLeuArglleTrplieLeuValLeuGinValA 218
                                                                                                                                                                                                                                                                                                                                                   296 yLeuLeuAsnGlnAsnPheArgLysGluTyrArgArgile 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 SerTyrTyrMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGl 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 erAspProAlaSerMetValProArgIleProGluTrpLeuPheValAla 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            937 Programment CATCHARD STOREST CATCHARD TO THE PROGRAMMENT AND COMPANY OF THE PROGRAMMENT OF THE PROGRAMME
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                                                                                                                                                                                                                                                                             61 a@lyAsnIlePheValValSerLeuAlaValAlaAspLeuValValAlaI 78
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alignment_scores:
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Ratio: 1.557
Percent Similarity: 59.104
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark 5
REGISTRATION NUMBER 37,259
REFERENCE/DOCKET NUMBER INTELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANI: Yu, Lei TITLE OF INVENTION: Mu Opinid Faceprines: Compositions and Mathods NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION NUMBER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             437 ACTCTATCGTGTGTGTGGGCCCTCTTCGGAAACTTCCTGGTCATGTAT 486
                                                                                                                                                                                                                                                                                                 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                            487 GTGATTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTT 536
                                                                                                                                                                                                                                                                                                                                                                                  367 GGGAACGACAGCCTGTGTCTCAGACCGGCAGCCCTTCC
                                        537 CAACCTTSCTCTGGCAGAC . GCCTTAGCGACCAGTACACTGCCCTTTC 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                  51 SerValTyrArqAsnLysLysLeuArqAsnAlaGlyAsnIlePheValVa 67
                                                                                                                                                                                                                                                        35 heThrile
84 alLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisCys 100
                                                                                                                                                                                                                                                                                                                                       19 pGlyAlaArgProSerTrpLeuAlaSerAlaLeuAlaCysValLeuIleP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1618 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                           3 GlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeuArqGlyAs 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY
                                                                               lSerLeuAlaValAlaAspLeuValValAlaIleTyrProTyrProLeuV 84
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512-474-7577
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214 1410
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                                                                                                                                                                                                                                                                                                 ...ATGGTCACAGCCATTACCATCATGGCCCCTCT 436
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:!!8-08-889-108-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 ......TrpLeuPheValAlaSerTyrTyrMetAlaTyrPheAsn 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       975 GATGATCTTACGACTCAAGAGC...GTTCGCATGCTALCGGGCTCCAAAG 1021
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                                                                                                                                                                                                                                                                                       321 alAspSerSerAsnAspValAlaAspArgValLysTrpLysProSerPro 337
                                                                                                                                                                                                                                                                                                                                                                                                                                            304 sGluTyrArgArgIleIleValSerLeuCysThrAlaArgValPhePheV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 lAlaSerAspProAlaSerMetValProArgIleProGlu....... 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 euLysPrcGlnAspPheArgAsnPheValThrMet PheValValPhe 244
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                                                                                                                                                 338 LeuMetThrAsnAsnAsnVal 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 SerCysLeuAsnAlaIleIleTyrGlyLeuLeuAsnGlnAsnPheArgLy 304
                                                                              ....ACGGCTAATACAGTG 1353
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                                                                                                                                                                                                                                                                                                                                                                                     ACCICATCCACGATCGAAC 1291
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; Sequence 3, Application US/08889108 ; Patent No. 6103492

GENERAL INFORMATION:

seq_documentation_block:

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alignment_block: 08 \cdot 09 \cdot 226 \cdot 046 \cdot 12 \times 08 \cdot 08 \cdot 889 \cdot 108 \cdot 3
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Ratio: 1.557
Percent Similarity, 59.164
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LOCATION: 3391.11235
-08-889-108-3
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TELEPAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAIIN: SYSTEM: PC-LOSYMS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                               "GAR CANCETTECTCTEGCAGAC"...GCCTTAGCGACCACTACACTGCCCTTTC 583
                                                                                                                                                  49 ' GTOATTGTAAGATACACCAAAAFGAAGACTGCCACCAACATCTACATTTT 536
                                                                                                                                                                                                                                                437 ACTOTATOOTOTATOTAGTGGGCCICHIGGGAAACHICCIGGICATGTAT 486
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PRIGR APPLICATION DATA:
APPLICATION NUMBER: OB, 2365, 518
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THTLE OF INVENTION: Mu optoid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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                                                                                           18ertenAlaValAlaAsptenValValAlaIleTyrProTyrProLeuV 84
                                                                                                                                                                                                 51 SerValTyrArgAssLysLysLeuArgAsnAlaGlyAssIlePheValVa 67
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"4 allouMetSerllePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisCys 100
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: 0.... 77210-4455
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Gaps: 12
Percent Identity: 25.770
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	CGGCTAATACAGTG 135	1339
	snVal 34	338
337	alAspSerSerAsbAspValAlaAspArgValLysTrpLysProSerPro	1292
	dSerLeuCysThrAlaA	304 1248
304 1247	SerCysLeuAsnAlaileileTyrGlyLeuLeuAsnGlnAsnPhoArqLy	298 1198
287 1197	TrpLeuPheValAlaSerT ::: coigecactionscarisci.	275 1154
274 1:53	spProAlaSerMetValProArqIleProG1	261 1122
261 1121	ValLeuPheAlaIleCysTrpAlaProLeuAsnPheIleGlyLeuAlaVa :::::: ::: ::: ::: ::::::::	245 1072
244 1071	eulysPioSlinAspPheArgAs:PheValThiMetPheValValPhe 	ри - В В В В В В В В В В В В В В В В В В В
229 1021	inA:4VallyscioAspA :: ::: gc gitcgcatgctat	212
212 974	lephedyslyrle CTGTGTGTTAC	196 934
195 933	ThrileAlaValVa ::: crecicaAAArcrererererererererererererererererer	x 12 x 8 4 4
184 883	roArgIle Addataing	167 ±34
167 833	uAlaAlaValLeuPro 	151 784
150 783	TSTYRASPLYSLeuTyrSerSerLysAsnSerLeuCysTyrValLeuLeu 	134 7:4
134 733	nlleThrGlyIleAlaIleAsnArqTyrCysTyrTleCysHisSerLeuL ::: :::::::::::::::::::::::::::::::	117 584
117 683	GlnValSerGlyPheLeuMetGlyLeuSerVallleGlySerIloPhoAs :::::: ANGA!GSPGA!GTCAATAGAITAG!AGAACA!GT!CAGCAGTATATTCAG	101 634
633	ACACHSTCANCHACCHSATGGGAACAHSSCCCHCGGAACCATCCTCTGC	584 4

seq_documentation_block:
 Sequence 1. Application PC/TUS9410358
 GENERAL INFORMATION:
 APPLICANT:

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, NAME/KEY: CDS
; LOCATION: 214..1410
PCT-US94-10358-1
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Patio: 1 557
Percent Similarity: 59.104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1618 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MI OPICID RECEPTORS: COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION DATA
PRIOP APPLICATION NUMBER: 08/120.601
APPLICATION NUMBER: 1993
TITING DATE: 13 SEPTEMBER 1993
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: IN TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEPHAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13 SEPTEMBE ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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CTTY: Houston
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                                                                                                                                                                                                                  437 ACTCTATCGTGTGTGTGGGGCCTCTTCGGAAACTTCCTGGTCATGTAT 486
                                                                                                                                                                                                                                                                                                                                                                                         367 GGGAACGACAGCCTGTGCCCTCAGACCGGCAGCCCTTGC.
                                                                                                                               487 STOATTOTANGATAGAGGAAATGAAGAGTGGGAGGAAGATGTAGATTTT 526
                                             537 CANCCTTSCTCTSSCAGAC SCCTTASCGACCAGTACACTGCCCTTTC 583
                                                                                                                                                                                                                                                    36 heThrIle ......ValValAspTleCouGlyAsnLouLeuValTleLeu 50
                                                                                                                                                                                                                                                                                                                                           19 pGlyAlaArgProSerTrpLeuAlaSerAlaLeuAlaCysValLeuIleP 36
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COMPUTER: IBM PC COMPOSTIBLE
OPERATING SYSTEM: PC-DOS/MS-LDOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                               67 | SerLeuAlaValAlaAspLeuValValAlaIleTyrProTyrProLeuV 84
                                                                                                                                                                    51 SerValTyrArqAsnLysLysLeuArqAsnAlaGlyAsnIlePheValVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER : FILING DATE: Concur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY .
84 alLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisCys 100
                                                                                                                                                                                                                                                                                                                                                                                                                             3 GlyAsnClySerAlaLeuFroAsnAlaSerClnProValLeuArgGlyAs 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON, MARK B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas
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                                                                                                                                                                                                                                                                                                           ATGGTCACAGCCATTACCATCATGGCCCCCC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 25.770
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seq_name: /cgn2_c/ptodata/2/ina,TCTUS_COME seg PoT-me94-10358-3
                                                                 seq_documentation_block:
Sequence 3, Application PC/TUS9410358 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1022 AAAAGGACAGGAATCTGCGCAGGATCACCGGGATGGTGCTGGTGGTCGTC 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 nileThrGlyIleAlaIleAsnArgTyrCysTyrIleCysHisSerLeuL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634 AAGATCGIGATCTCAATAGATTACTACAACATGTTCACCAGCATATTCAC 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GlmValSerGlyPheLeuMetGlyLeuSerVallleGlySerIlePheAs 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                584 AGAGTGICAACTACCTGATGGGAXCACGGCCCTTCGGAACGATCCTCTGC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 AGACCGTITCCTGGCACTTGTGCATTGCT.....TTGGGTTACACGAAC 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 AAGCCCTGGATTTCCGTACCCCCGGAAATGCCAAAATCGTCAACGTCTGC 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       684 CCICTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACCCAGTCA 733
                                                                                                                                                                                                                                                                                                                                                                                                                             1248 ATGCITCAGAGAGTTCTGCATCCCA.....AUCIDSICCAPGATGGAAC 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1198 AGCTGCCTGAATCCAGTIUTITACGUCTTCCTGGATGAAAACTTCAAGCC 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1072 GCTGTATTTATCGTCTGCTGGACCCCCATCCACCATCTACGTCATCATCAA 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 834 CACAAAATACAGGCAGGGGTCCATAGATTGCACCCTCACGTTCTCCCCACC 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           784 AACTGGATCCTCTTCTGCCATCGGTCTGCCTGTAATGTTCATGGCAAC 833
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                                                                                                                                                                                    1339 .....ACGGCTAATACAGTG 1353
                                                                                                                                                                                                                                                                                                          1292 AGCANAACTCCACTCGAGTGGGTCAGAACACIÁ3GGAACATCCCTCC... 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 ValLeuPheAlaTleCysTrpAlaProLeuAsuPheTleGlyLeuAlaVa 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 eurysProGlnAspPheArgAsnPheValThrMet ...PheValValPhe 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            975 GATGATCTTACGACTCAAGAGC...GTTCGCATGCTATCGGGCTCCAAAG 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 eLeuValLeuGlnValArgGlnArgValLysProAspArgLysProLysL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  934 TICATCATGCCGATCCTCATCATCACTGTGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 PheLeuValProMetIleIleValIlePheCysTyrLeuArgIleTrpIl 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        884 CAACCTGGTACTGGGAGAACCTGCTCAAAATCTGTGTCTTTATCTTCGCT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 erSerAlaTyr......ThrIleAlaValValValPheHis 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 SerCysLeuAsnAlaTleIleTyrGlyLeuLeuAsnGlnAsnPheArgLy 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 ......TrpLeuPheValAlaSerTyrTyrMetAlaTyrPheAsn 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 sGluTyrArgArgIleileValSerLeuCysThrAlaArgValFhcFhcV 321
                                                                                                                                                                                                                                                                                                                                                                  521 alAspSerSerAsnAspValAlaAspArgValLysTrpLysProSerPro 337
                                                                                                                                                                                                                                               338 LeuMetThrAsnAsnAsnVal 344
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APPLICANT

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alignment_block:
-08-09-226-046-12 x PCT-US94-10358-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 328.50 Length: 357
Ratio: 1.557 Gaps: 12
Percent Similarity: 59.104 Fercent Identity: 25.770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seq 1/1 for prof-11844-18458-4 from: 1 fo: 1518
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TELEX: 79-0924
INFORMATION FOR SEQ ID NOT
                                                  5.47 CAACCTTGCTCTGGCAGAC...GCCTTAGGGAGGAGTAGAGTGGGGTFFC 58%
                                                                                                                                                  487 OTGATTGTAAGATAGAGGAAAATGAASAGTGCCAGCAACATGTAGATTTI 536
                                                                                                                                                                                                                                                     4 0 ACTOTATOGICIOTOTAGIGOGOTOTICGGAAACIICGIGGICATGTAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-7 GGGAACGACAGCCTGTGTGCCCTCAGACCGGCAGCCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MULECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/POCKET NUMBER: INTELECTATION INFORMATION TELECHMONIC (712) 418-3000 TELEPAX: (715) 289-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTOMBUSACETY TABLE SEPTEMBE ATTOMBUSACION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                13 ISerteuAlaValAlaAspLeuValValAlaIleTyrProTyrProLeuV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "URRENT APPLICATION DATA: PCT/US94/10358
                                                                                                                                                                                                     '! SerValTyrArqAsnLysLysLeuArqAsnAlaGlyAsnIlePheValVa 67
84 alLouMotsorlloPhoAsnAsnGlyTrpAsnLouGlyTyrLouHisdys lûû
                                                                                                                                                                                                                                                                                                     (6 heThrile.....ValValAspileLeuGlyAsnLeuLeuValileLeu 50
                                                                                                                                                                                                                                                                                                                                                                                                        TH polyAlaArdProSerTrpLeuAlaSerAlaLeuAlaCysValLeuIleP 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/120.501 FILING DATE: 13 SEPTEMBER 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
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OPPRATING SYSTEM: PC-DOS/MS-DOS/ASCII
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                                                                                                                                                                                                                                                                                                                                                             ATGGTCACAGCCATIACCATCATGGCCCTCT 436
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1122 Accc
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                                                                                                                                                                        338 LeuMetThrAsnAsnAsnVal 344
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ACGGCTAATACAGTG 1353
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seq_documentation_block:

Seguence 6, Application US/08351473B Patent No. 5656440

GENERAL INFORMATION:

seq_name: /cgn2_5/ptodata/2/ina/5A_c0Mb.seq:Us-08-351-473B-6

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TOPOLOGY: linear (MALECULE TYPE: UNA (MALECULE TYPE: UNA (MALECULE) US-08-351-4738-6
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REFERENCE, DONKET NUMBER 5633
TELECOMMUNICATION INFORMATION.
TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEPAX: (703) 413-2220
TELEX: 248955 CFAT UP
INFORMATION FOR SECTION: (6)
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: Single
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-351-4738-6 from 1 to: 1218
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COMPUTER PRADABLE FORM:

REDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-TA/S

SOFTWARE: PATENTIN PC-DOS/MS-TA/S

CURRENT APPLICATION DATA:

APPLICATION NUMBER: TS/OR/351.4738

FILING DATE: 21-FFB-195

CLASSIFICATION: 435

CLASSIFICATION: 435

FILING DATE: 21-FFB-196

FILING DATE: 21-AFP-196

FILING DATE: 21-AFP-196

APPLICATION NUMBER: 93 04570

FILING DATE: 21-AFP-1964

APPLICATION NUMBER: PCT/FF94/00447

FILING DATE: 21-AFP-1964

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CORPESPONDENCE ADDRESS:
                                                                                                                              169 CTGGTAATCGTGGCCATCCCCGGACGCCGAGACTCCAGACCATGACCAA 218
                                                                                                                                                                                                                                                                                                       119 COGGGGGCTGTTGGGGGCTAGGGGTGGTGGGGAGGCAACCTG 168
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                                                                                                                                                                                                         47 LeuValIleLeuSerValTyrArgAsnLysLysLcuArgAsnAlaGlyAs 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 ТАСТОССААСОСАСТОВОТОВСТВОСАВОВОТОГСТВОВСЕВСТВОСТВО 118
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63 nIlePheValValSerLeuAlaValAlaAspLeuValValAalaILeTy=P 80
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KAPOOR, ARCHANA
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Percent Identity: 26.016
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315	299 1045	282 998	267 963	251 913	234	228 913	on.	12 12 13	219 713	204 663	188	175	163 : 519 :	147 7 469 0	130 S	113 y 369 č	97 T	1 697 1 08	D 613
	ASDGINASUPhoArgLySGLuTyrArgArg11eIleValSet;eucTysT ::: :::	2 yrMetAlaTyrPheAsnSerCysDeuAsnAlaTleTlcTyrGlyDeuLeu ::::::: ::::: 	zMetVal	II palaproLeuasnPheileGlyLeuAluvalAlaScrAspFtoAlaS 	4 heArgAsnPheValThrMetPheValValPheValLouPheAlaIleCys	Line Line	TCTCGCTCCGGAT	•	TGCGCCGGGAGCTGGGTGGCTTCCCCCCAGAGAGAGTCTCTGTGTTGGCTTCT	eFhecysTyrLeuArgIlcTrpIleLouValLou	ThrileAlaValValValPheHisPheLeuValProMctileIleValIl	yrser	argalaglyThrLeuGlnTyrAspProArgIleT	TyrValLeuLeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLe ;;; ;; couTuaTccToGTGTGGGTGTGTCCCCCCGGGTGTCGTTTGCCCCAT	ysHisSerLeuLysTyrAspLysLeuTyrSerSerLysAsnSerLeuCys	ySerIlePheAsnIleThrGlyIleAlaIleAsnArgTyrCysTyrIleC 	TyrLeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerVallieGl	roTyrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGly	GAGCTCCTO
	h 315	1 298	T 282	9 S	912	234 952	812	13	227 762	218 712	204 662	187 519	5 7	163 518	146 468	130 418	113 368	96 318	258

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TILLING ICALL.

TILKSIFICATION 435

FRITE APPLICATION NUMBER: 93 04670

FILLING DATE: 21 APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PGL/FF44/C0447

FILLING DATE: 21 APR-1994

ATTOPNEY/AGENT INFOPMATION

NAME: ORLON, NORMAN F.
FREISTFALITON NUMBER: 6639-001-0X PCT

TELEFORMMYSICATION SEPENATION:
TELEFAX: (703) 413-3000

TELEFAX: 248855 OPAT UR
INFOPMATION FOR SEP ID NO. 1.

**TO-UNDERSOR OF ALTHORY OF ALTHORY
FREEX: 248855 OPAT UR
INFOPMATION FOR SEP ID NO. 1.
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                                                                                                                                                                                                                                         alignment_block
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                                                                                                                                                                   Allyn sed 1/1 to: 88 68 (51:47:90) from: 1
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                                                                                                                                                                                                                                                                                      Percent similarity:
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AFFLICANT: LENZEN, GERLINDA
AFFLICANT: KAPO-P ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: HOVINE BETAR-ADBRENERGIC PECEPTOR AND THEIR APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READARLE FORM:
MEDIUM INFE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-POS/MS-POS
SOFTWARF: PATENTIE Pelease #1.0, Version #1.40
CURRENI APPLICATION DATA:
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(***PRESPONDENCE ANDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT STREET: 1755 5 TEFFERSON DAVIS HIGHWAY, SUITE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOSTECULE TYPE: DNA (denomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: FORCE C
                                                                      125 GOGAACAGCTCTCTGACCCCGTGGCCAGATATCCCCACCCTGGCACCCAA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
hami, Eff. 313
LOCATION: 107..1821
THEP INFORMATION: Afgrostion= "ROVINE RETA-'S RECEPTOR"
OTHER INFORMATION: Appoint = "ADMENERGIC, BETA PECEPTOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/351,473B FILING DATE: 21-FEB-1995
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CITY: ARLINGTON
STATE: VIRGINIA
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                                                                                                                   GlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeuArgGlyAs 19
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Maximum DB seq length: 200000000
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                            Database
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1505
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Match Length
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Gapop 10.0 , Gapext 0.
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Listing first 45 summaries
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(c) 1993 - 2000 Compugen Ita
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Mel-ic receptor su
melatonin receptor
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la melatonin r
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RESULT 138848 Mel-la; C:Speci C:Date: C:Acces R;Reppe Neuron A;Title A;Refatu A;Statu A;Mesid A;Cross C;Super		00000000000000000000000000000000000000
MESULT 1 138848 Mel-la melatonin receptor - human (receptors (man)) Crispecias: Homo sapiens (man) Crispecias: Homo sapiens (man) Crispecias: Homo sapiens Crispecias: Homo sapiens Crispecias: Homo sapiens Crispecias: Homo sapiens Meaver, D.R.: Ebisa Respect, S.M.: Weaver, D.R.: Ebisa Neuron 13, 1177-1185, 1994 A;Title: Cloning and characterizati A;Title: Cloning and characterizati A;Reference number: 138848; MUID:95 A;Reference number: 138848 A;Status: preliminary; translated f A;Molecule type: mRNA A;Residnes: 1-350 (FRES) A;Cross-references: EMBL:U14108; NI C;Superfamily, vertebrate rhodopsin		306.5 305.5 305.5 305.5 305.5 305.5 305.5 305.5 305.5 305.5 305.5 305.5
n recept sapiens sapie		116.577
septor human lens (man) #sequence_revision #sequence_revision aver, D.R.; Ebisawa 5, 1994 characterization d characterization 138848; MUID:95033 ry; translated from NA RES> EMBL: U14108; NID:9 cbrate rhodopsin		33455 33455 33455 33664 33663 3663 3663
human) ;e_rev ?: Et ?: Et ?: Et !eriza MUID: MUID:		инининининини
RESULT 1 138848 Mel-la melatonin receptor - human Mel-la melatonin sapiens (man) C:Species - Homo sapiens (man) C:Species - Homo sapiens (man) C:Species - Homo sapiens - human Mel-la melatoning - Helical - Helical - Helical Mel-la melatoning - Helical Mel-la mel-	ALIGNMENTS	A45490 836794 829248 829248 841795 812863 812863 841795 84227 847294 772940 772940 772949 7407449
sion 2y-May-1y38 #text_change 29-Apr-2000 Lsawa, T. Lion of a mammalian melatonin receptor that mediates 95033233 from GB/EMBL/DDBJ from GB/EMBL/DDBJ	MENTS	neuropeptide Y/pep beta-1-adrenergic alpha-1-adrenergic somatostatin recep alpha-1B adrenergi somatostatin recep G protein coupled neuropeptide Y/pep somatostatin recep delta opioid recep neuropeptide Y rec somatostatin recep somatostatin recep somatostatin recep brain-specific som histaniha. M2 recep

gg	K)	90	Qy	Db	Qy	da	7.0	מת	Qy	Dβ	Qy	Bes	0110
301 NERKEYRRIIVSLCTARVFFVDSSNDVADRVKWKPSPLMINNNVVAVUSV 500	301 NEFFEYRPITVSEATARVEFVDSSNDVADRYKWKPSPLMINNNVVKVDSV 350	101111	241 FVVFVLFAICWAPINFIGLAVASDPASMVPRIPEWLEVASYYMAYENSCHRAIIFGLING 300		181 QSVSSAYTIAVVVEHELVEMIIVIECYLERIWILVLÜVELEVEREKEKEKEZOPERIVIM 240						1 MQGNGSALPNASOPVLRGDGARPSWLASALACVLIFTIVVDILGNLLVILSVYRNKKLRN 60		T00.0%;

Mel-la melatonin receptor - sheep C.Spocios: Ovis orientalis aries. Ovis ammon arios (domestic sheep) C.Dato: 19-Dec-1997 #sequence_revision ly-Dec-1997 #text_change 17-Mar-2000

RESULT 145469

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A:Molecule type: mkNA
A:Residues: 1-420 <EBI>
A:Gross::eferance: ""
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R:Repport, S.M.: Weaver, D.R.: Ebisawa, T.

Nouron: 13, 1177-1185, 1994

A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates A:Retorence number: 138848; MUID:95033233

A:Accession: 146469
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C:Superfamily: vertebrate rhodopsin
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A:Molecule type: mRNA
A:Residues: 1-366 <REP>
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                                                                                                                                                                                                                                                              Swery Match

58.5% Score 1244: 58.2;

Best Local Similarity 70.4% Pred. No. 7.7e-96;

Matches 224; Conservative 52; Mismatches 42;
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146 CYVILIMITTI AAVI PNI PAGTI QYEPFIYSGTFAQSVSSAYTI AVVVEHFI VPMIIVIF 205
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                                                       *1 TALEGNOWTLONIHOGISGELMGLSVIGSVENITATAINFYCYTCHSLFYDKLYNGESTW 150
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                                                                                                                                                          3 LTSALAVVLIFT[VVDVLGNILVILLSVLRNKKLQNAGNLFVVSLSIADLVVAVYPYPVIL 90
                                                                                                                                                                                                            26 TASATACVI IFTTVVDTI GNILLVILSVYBNKKLPNAGNIFVVSLAVADLVVATYPYPLVL 85
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                                                                                                      MSIFNNOWNLOYLHOOVSGELMGLSVIGSIFNIIGIAINEYCYICHSLKYDKLYSSKNSL 145
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81.3%; Pred. No. 1.5e-117;
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A:Cross-references: EMBL-030004; NID:glu50952; PID:glu50963 R.Liu, F., Yuan, H., Suyamori, K.S., Hamadanizadeh, A.: Loc, F.J.S.: Pang, S.F.: Bir: FERS Left 374, 273-278, 1995 A:Title: Molecular and functional characterization of a partial cDNA encoding a novel A:Reference number: S68240; MUID:96063731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: preliminary, nucleic acid sequence not shown A:Molecule type: mRNA A:Posidaes: l=f3, f5-290 cIIUs A:Cross=references: EMBL:U30609 C:Superfamily: vertebrate rhodopsin
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A; Molecule type: mRNA
A; Residues: 1-289 <NIZ>
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C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
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                                              19. TEKEYERTIVSI/TIARVEEVI/SSNEVALEVKWKESPLMTNNNVVKVDSV 350
                                                                                                                                                             242 VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIIYGLLNQN 301
                                                                                                                                                                                                                    326 DVADRVKWKPSPLMTNNN 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 FHVAFKIFEMLFVLSÝFMÁYÉNSCINAVIYOVINQNEKKEYKRILMSLLTPRII FIDTSE 330
                                                                                                           181 VVEVIEAFCWAFLNEIGLAVAINESEMARKVEBWLEIISYEMAYENSCLNAIIYGLLNÛN
                                                                                                                                                                                                                                                                      182 SVSSAYTIAVVVEHELVPMILVIEGYLRIWILVLQVEQEVKEDEKPKLKPQDERNEVTME 241
                                                                                                                                                                                                                                                                                                                                                                                    LEZ ALNEYSYLSHSSKYSKIYSSKNSISYVILIWILLICAAVLENDRASILGYSEFTYSSTEAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GNIPVVSLAVADLVVAIYPYPLVLMSIENNOWNIGYLHCQVSGFLMGISVIGSIENITGI 121
                                                                                                                                                                                                                                                                                                                                   61 AINRYCYICHSFAYDKVYSCWNTMLYVSLIWVLTVIATVPNFFVGSLKYDPRIYSCTFVQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S72554; S68240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.7%; Score 1119; DB 2; Length 289; 69.9%; Pred. No. 1.2e-85; ative 42; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saps
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Mellb-melatonin receptor - human C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 31-May-1996 *sequence_revision 31-May-1996 *text_change 17-Mar-2000 C:Paccession: 138990

A-Status: preliminary: translated from GR/EMBL/DDBJ A:Molecule type: mRNA A.Kesidees: 1-362 <PES> A-Cross-references. EMBL:U25341: NID:qy71193, FIDN:A Cross-references EMBL:U25341: NID:qy71193, FIDN:A

Local Similarity

205;

Cross_references. EMBL:U25341: NID:g971193, FIDN:AAC50612 1: PTD-g971194

B

3 GNGSALPNASQPVLRGDGARPSWLASALACVLIFTIVVDILGNLLVILSVYRNKKLRNAG 62

Conservative 52; Mismatches 70;

59.9%;

Score 1088; DB 2; Length 362: Pred, No. 5.7e-83;

Indels

76 NLELVSLALADLVVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIA 135

g Ŷ

INRYCYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLPNFFVGSLEYDERIYSCTFTCT 195

INPYCYICHSLKYDKLYSSKNSLCYVLLIWLLILAAVLPNLRAGTLOYDPRIYSCTFAQS 182

Ş g G

g

R;Reppert, S.M.; Weaver, D.R.; Ebisawa, T.; Mahle, C.D.: Koldkowski Jr., b F FB3S Lett. 386, 219-224, 1996 A;Fitle: Oloning of a melatonin-related receptor from human pituitary. A;Feference number: \$70520; Mult 962199069 A;Accession: \$70520

A:Status: preliminary: nucleic acid sequence not shown A:Molecule type: mRNA A:Pesidues: 1-613 <PEP>

A:Cross-references: EMBD:U52219: NID 41326154; PIDN-AAU59614.1: PID.41226155

C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 *sequence_revision 13-Mar-1997 *text_change 05-Nov-1999
C:Accession: \$70520

melatonin receptor homolog - human

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R.Reppert, S.M., Godson, G. Mahle, G.D. Wonver, D.F.; Slaudenhaupt, S.A.; Gusella, J.F. Proc. Natl. Acad. Sci. U.S.A. 92, 8734-8738, 1995
A.Title: Molecular characterization of a novel melatonin receptor expressed in human ret A.Reference number: 138990; MUID:96004613
A.Reference number: 138990; MUID:96004613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melatonin receptor - striped hairy-footed hamster (fragment)
C:Species: Phodopus sungorus (striped hairy-footed hamster)
C:Date: 04-Sep-1997 *sequence_revision 07-Nov-1997 *text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Reppert, S.M., Weaver, D.R.; Ebisawa, T.
Neuron 13, 1177-1185, 1994
A;Title: Cloning and characterization of a mammalian melatonin receptor that mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U14110; NID:g0U2133; FID:g0U2134 C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: 138848; MUID:95033233
A;Accession: 184498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: mRNA
A; Residues: 1-156 <PES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuron 13, 1177-1185, 1994
Ay.Title: Cloning and characterization of a mammalian melatonic recoffor that mediates Ay.Reference number: 138848; MUID:95033233
AyAccession: 162107
A.Gression: 162107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Moseldues: 1-156 :PESN
A;Residues: 1-156 :PESN
A;Cross references: EMBL:U14409; NID:g602135; FIDN:AAA57131.1. PTC q602136
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/EDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 PVETVTIVCIHEVLELLIVGECYVEIWTXVLAARD--PAGUNEUNULAEVKHELIMEVIT 247
                                                                                                                      Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 LIFAVCWCPINVLTVLVAVSPKENAGKIPNWLYLAAYFIAYENSCLNAVIYGLLNENPPP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 VLEAICWAPLNEIGLAVASDPASMVPRIPEWLEVASYYMAYENSCLNAIIYGLLNONERK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 EYWTIFHAMRHPIIFFPGLISDIRE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 CYICHSLKYDKLYSSKNSLCYVLLIWILITLAAVLPNLRAGTLOYDPRIYSCTFAOSVSSA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 YTIAVVVEHELVPMIIVIECYLRIWILVLQVEQPVKPDPEKPKLKPQDERNEVTMEVVEVL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 FAICWAPLNEIGLIVASDPATMAPRIPEWLEVASYY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 FAICWAPLNEIGLAVASDPASMVPRIPEWLFVASYY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 89.1%; Pred. No. 1.96 es 139; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YTTAVVVEHETVPMITVTECYLRIWILVLOVEREVKEDSKFELKPODERNEVTMEVVEVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CYTCHSLKYDRLYSNKNSLCYVFLIWVLTLVAIMPNLQTGTLQYDPRIYSCTFTQSVSSA 60
                                    127 GYTOHSLKYDKLYSSKNSLGYVLLIWLLTLAAVLPNLRAGTLQYDPRIYSCTTAGSYSSA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYRPITUSLCTARVFFVDSSNDVAD 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                    Local
MARIA DEL PARTE SALVE DE LE COMPUNE DE LA CO
                                                                                                                                                               th 41.4%; Score 751; DB 2; Length 156; Similarity 87.2%; Prod. No. 2.2c-55;
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.1%; Score 764; DB 2; Length 156; 89.1%; Pred. No. 1.9e-56;

    Mismatches

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Query Match
Local Similarity
                                                                                                                                                                                                 5 GSALFNASQPVLRGDGARPSWLASALACVLIFTIVVDILGNLLVILSVYRNKKLRNAGNI 64
                                                                                                                                                           GCKLPOPEYP-----PA-LIIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNI 65
                                     RYCYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTLQYDPPIYSCTFAQSVS 184
                                                                               FVVSLSVADMLVAIYPYPLMLHAMSIGGWDLSQLQCQMVGFITGLSVVGSIFNIVAIAIN 125
                                                                                                                    FVVSLAVAELVVAIYFYFLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIAIN 124
                                                                                                                                                                                                                                           49.1%; Score 891.5; DB 2, Length 613; ilarity 49.5%; pred. No. 1.9e-66; conservative 71: Mismatches 82; Indels 11
                                                                                                                                                                                                                                                              Indels 11; Gaps
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В

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K:LOTIMET, D.D.: Matkowsk), K.; Menya, R.V.
Riochem, Riophys, Res. Commun. 241, 558-564, 1997
A:Trile, Cloning, chromosomal location, and transcriptional regulation of the human gala A:Reference number: JC5801; Mulli-чилинской
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Molecule type mRNA
A:Pesidues: 1-349 < LDF
A:Cross-references. GR.753511, NID 91297337; FIDN:
A:Note: submitted to the EMBL Data Library, April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C)Date: 31-May: 1335 *sogleneb_revision 11-May:1395 *text_change 21-31-2770 C)Date: 31-May:1395 *text_change 21-31-2770 C)Accession: 159386; JC5801; G01765; G02528 C:Rahert-Ortoli, E. Amiranoff, B. Edwardt, F.: Laburthe, M.; Mayaux, J. Proc. Natl. Acad. Sci. U.S.A. 91, 9780-9783, 1994 A:Title: Molecular cloning of a functional human galanin receptor. A:Reference number: 159336; MUID:95024044
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C:Superfamily vertebrate :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Cross-references: EMBC-723844: NID:q775209: FID:q775210
C:Comment: This receptor inhibits cAMP formation, stimulates and inhibits phospholipose, and increases arachadumic acid metabolism, as well as opens AIP-dependent K- but close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    As Reference number, G08350
As Accession: G01765
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A; Residues 1:14, 'W', ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMRL Data Library, March 1995
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A:Cross-reterances- GR:134339; NID-q559047; PIDN-AAA50767 1; PID-g559048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references | GDB-392699; | QMIM:600377
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Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acression: 159336
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THE NOTEGWEOWERSKHKKAYVVCTEVECHTEDETTIEFTYAKV---ENHIHKKEK-NMSKKS ZER
                                                                                                                                                124 FTHAAMSVDRYVAIVHSRPSSSLRVSRNALLGVGCIWALSIAMASPVAYHQGL-FHPRAS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 FALCWAPLNEIGLIVASDPATMAPRIPEWLFVASYY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
                                                                                                                                                                                                                      216 ENITGIAINRYCYICHSLKYDKLYSSKNSLCYVLLIWILTHAAVLPNLRAGTIQYDPRIY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 FAIGWAPENFIGLAVASDFASMVFRIFEWEFVASKY 282
                                                                                                                                                                                                                                                                                                64 OKPRSTTNIFILNUSIADLAYLLEGIPEQATVYALPTWVLGAFIGKFIHYEFTVSMLVSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YTIALVVEHEVVEMTIVTECYLRIWILVLQVEREVKENESKEKLKEGDEENEVTMEVVEVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                          57 -KLRNAGNIEVVSLAVADLVVAIYPYPLVLMSIENNGWNLGYLHOQVSGELMGLSVIGSI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                        10 BONASCEEPPAPEPGEPLEGIG · · · · · VENEVILVVEGI IFALGVIGNSLVITVLAPSKE (3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QONGSA-LPNASQP-VLRGDGARPSWLASALACVLIETIV--VDILGNLLVILSVYRNK- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTCHSLKYCKIYSUKNSCCYVELLWILLILIAIMPNLLIGILQYDPRIYSCTETQSVSSA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTTAVVVEHELVPMITVIFCYLRIWILVLQVRQRVKPERKPKLKPQEFRNEVIMEVVEVL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 18.5%; Score 335; DR 2;
Similarity 29.2%; Pred. No. 1.6e-20;
95; Conservative 67, Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The translate the disposit
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                                                                      SSAYTIAVVVEHELVEMIIVIECYLEIWILVLQVEGEVKEGEKEKC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIP.g1297337; FIDN: NACS1936.1; FID:g1297338
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more Pharmacol 44, 8-12, 1993
A;Ittle: Molecular cloning and functional expression of a morepiold receptor from rat
A;Accession: 157951
A;Status: prailminarus see:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Experimental source: brain membranes
A:Note: sequence extracted from NCBI backbone (NCBIP-140841)
B:Sodq! M. Poys F: Parakrishnan, S: Eldo. B: Loh, H.H.
B:Johlen Blophys Res Commun. 129, 563-574, 1995
A.Title: Complementary UNA closing of a municipied disceptor from rat pertitioned macrop A:Reference number: I52314; MUID:95251654
A.Accession: I52314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc Natl Acad Sci W.S.A. 90, 10230-10234, 1993
A:Title: Mu object receptor obNA cloning and expression.
A.Beforence number A48799, MUTD 94052137
A:Accession: A48799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: Sprague Dawley, peritoneal macrophages F: Fikida K ; Kato S ; Mori, K ; Nishi, M.; Takeshima, H. FEBS Lett. 327, 311-214, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: protein
A;Posidues: 272-291 <EFF>
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R;Eppler, C.M.; Hul
T Riol Chom 268,
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A:Molecule type: mRNA
A:Residues: 1-348 <PE2>
                               R:Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J. Neuron 11, 903-913, 1993
                                                                                                                        A;Status: preliminary; translated from GB/FMBI/DDBJ (A;Molecule type: mBNA)
A;Residues; 1-244,/V/,246-398 <WANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: S34592; MUID:93351652
A;Accession: S34593
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A; Mesidues 1:398 < PE
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A:Aggession, I56517
A; Title: Cloning and pharmacological characterization of a rat mu opicid receptor
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references. GB:Dib345, NID:3391866, PIDN.BAA03852 1, FID g>33857
R:Wang, J
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A;Pesidues 1:244,'V',245 398 :EUK/
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A; Cross-references: GB:877863; NID:9998546
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                                                                                                    A) Cross-references - GB-L25684;
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268, 26447-25451, 1993
                                                                                                    NIL-g409149; FILW:AAA41543.1; PIF-g409150
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Tue Feb

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A:Gene: MOOR1
C:Superfamily: vertebrate rhodopsin
C:Keywords. G protein coupled receptor: transmembrane protein
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A;Residues: 1-244,'V',246-398 <THO>
A;Residues: 1-244,'V',246-398 <THO>
A;Croos*references: JB.LL2455; NID 3437671: FID:a437672
C:Genetics:
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A:Status: preliminary: translated from GR/EMBL/JDBJ
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C:Species: Pattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
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R;Zastawny, R;L., George, S.R.; Nguyen, T; Cheng, R.; Tsatsos, J; Briones-Urbina, R.;
R;Zastawny, R;L., George, S.R.; Nguyen, T; Cheng, R.; Tsatsos, J; Briones-Urbina, R.;
R;Zastawny, R;L., George, S;R.; Nguyen, T; Cheng, R.; Tsatsos, J; Briones-Urbina, R; A; Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rat brain, Title: Cloning, Characterization, and distribution of a mu-opioid receptor in rate brain, Title: Cloning, Characterization, and C
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A: Residues: 1-398 < RES
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A:Accession: 156504
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                                                                                                                            102 ATNIYIENLALAD-ALATSTLEFQSVNYLMGTWPFGTILCKIVISTDYYNMFTSIFTLCT 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match. 18.0%; Score 326.5; DB 2; Length 879; Local Similarity 25.9%; Frod. Nc. 9e-20; Local Similarity 76; Mismatches 148; Indels 39; Gaps 92; Conservative 76; Mismatches 148; Indels 39; Gaps
                                                                                                                                                                                                                         51 AGNIFVVSLAVADIVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNIIG 120
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                               IAINRYCYICHSLEYDKIYSSENGICYVILLIWLITIAAVIEWLPAGTIQYOPGIYGCIFA 180
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Fred No. 9e-20;
DB 2; Length 398;
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198
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R;Murphy, L.: Harris, D.; Barrell, B. submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanocaster.
A;Reference number: Z17668
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C:Species: Drosophila melanogaster
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C:Accession: T13739
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A; Note: EG:22E5.11
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A residues: 1-670 <MTR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 FSHPTWYWENLLKICVGIFAFIMPVLIITVCY---GLMILRLKS-VRMLSGSKEKDPNLR 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 LNPVLYAFLDENEKRCFREECIP--TSSTIEQONSTRVRONTREHPS---TANTV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 RITRAVLVVVAVEIVCWTPIHIYVIIKA-----LITIPETTFQTVSWHFCIALGYTNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 NEVIM-EVVEVLEAICWAPLNEIGLAVAS: PASMVPPIPEWLF VASYY----MAYENSC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 LNALIYGILNZNERKEYRFIIVSIGTARVFEVDSSNEVADRVKWKRSPLMINNNV 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                    159 ACWLESYGNCLETTLIGEWAPERYDSPLOTESINTDDHGHSKTTLETTA--EVIPCLVII 216
                                                                                                                                                                                                                                                                                                                                                                                                                    150 LIWLLTLAAVLPNLRA--GTLQYDPRIYSC---TFAQSVSSAYTIAVVVFHFLVPMIIVI 204
                                                                                                                                                                                                                                                                             217 ACYAKIFWYYHKSEQELKEHATYQUSIPNMLPPLASTGSGALPSGAECOPSNRVSSDSSS 276
                                                                                                                                                                                                                                                                                                                          205 FCYLPIWILVIQVRQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                 262 ASDPASMVPRIPEWLFVASYYMAYENSCLNAIIYGLLNUNFKEYPRIIVSLC TARVFF 320
                                                                                                                                                                              277 SESIDVEETAPSGKQQETFVKDQPEVPAKPNEWPITKMVLAIFLSFVVCYLDITIVKVA- 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 AAVMTELIMIVGICGNLLTVVALLKCPKVRNVAAAFIISLCIADLLECALVLPEQGLREV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 PFGKTNGASSAAE--KWKDIGLSNNHS 412
                                            321 ----VDSSNDVADRVKWKPSPLMTNNN 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 QGTWPHQQVLCRLIPFIQYGNLGVSLLCIAMITINRYVMITHHGLYARIYKRHWIAVMIA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 NNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIAINRYCYICHSLKYDKLYSSKNSLCYVL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSVSSAY----TIAVVVEHELVPMIIVIECYLRIWILVLQVRQRVKPDRKPKLKPQDER 235
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                                                                                         --DKNVEHFS----LHICSYILLYESACINETTYVIMMKQYPKAYKTVV--FCQPARLLL 387
                                                                                                                                                                                                                                17.9%; Soure 325.5; DB 2; ilarity 23.8%; prod No. 1.8e-19; conservative 69; Mismatches 139;
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beta-40-adrenergic receptor - turkey C;Species: Meleagris gallopavo (common turkey) C;Late: 18.Nov-1394 #Sequence_10015: 8 18-3 %-1004 #*fixt_chingo 13-Aug-1000

A; Accession: S31659 A; Status: preliminary A: Molecule type: DNA

meutotransmitter receptor:

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submitted to the RMBC Sata Library, June 1992.
A:Description: Rowins betak adrenorale receptor, partial genomic sequence
A:Reference number: $31659
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A:Status: nucre...
A:Molecule type: DNA
Finaldues: 162-298 <CAS>
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CySpecies: Nos primigenius taurus (cattle) 
CySpecies: Nos primigenius taurus (cattle) 
Cybrid - 28-oct-1946 *sequence_revision 13-Mar-1997 *text_change 13-Aug-1999 
CyAccession: S65499; S40504; S31659 
RePietri-Rouxe), Fr. Lenzen, G.: Kapcer, A.: Drumare, M.F.: Archimbault, P. 
Bur, J. Blochem, 230, 350-358, 1995
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R:Chen, X.: Harden, T.K.: Nicholas, R.A.
J. Biol. Chem. 269, 24810-24819, 1994
J. Biol. Chem. 269, 24810-24819, 1994
A:Title: Molecular cluding and characterization of a novel beta-adieneryle receptor A:Reforence number: A55044; MUID-95014249
A:Accession: A55044
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A:Residues: 1:428 ciHbe
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Fred. No. 1.3e-19
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A,FA:Alaes, 4-5, HE', 8 105 Y870>
A.Gross-references: EMBL:X67214
C:Superfamily: vertebrate rhodopsin
C.Keywords, 0 probein coupled
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C. Reportantial Control of Control of Symptotic neutronalsmitte E 37-70,75 main transmembrane #status predicted sTML E 73 101,75 main transmembrane #status predicted sTML E 73 101,75 main transmembrane #status predicted sTML E 156-173,75 main transmembrane #status predicted sTML E 156-173,75 main transmembrane #status predicted sTML E 154-175,75 main transmembrane #status predicted sTML E 153-314,75 main transmembrane #status predicted sTML E 151-141,75 main transmembrane #status predicted sTML E 153-314,75 main transmembrane #status predicted sTML E 158-3141,75 main transmembrane #status predicted sTML E 158-3141,75 main transmembrane #status predicted sTML E 158-3141,75 main transmembrane #status predicted E 
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A:Accession: 002953
A:Accession: 002953
A:Stalls: preliminary, translated from DE/TMET/CDET
A:Molecule type: DNA
A:Ecsidues: 1:418 (1904)
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GIDATE: Il Dec-1996 #sequence_revision 06 Jun:1997 #text_change 13-Aug-1999
GIACCESSION: GO2953
RIDOWE, A.L., Walston, J.; Shuldiner, A.R.
submitted to the EMBL Date Library, July 1996
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C:Superfamily: vertebrate rhodopsin
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PROSITE: PS00247;
                                                                                      MLIA_PHOSU STANDARD, PRT. 353 AA PA-1217; PRT-1217 (Rel. 83, Created) 01:NOV:1997 (Rel. 85, Last sequence update) 15:JUL-1998 (Fel. 85, Last annotation update)
Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
Eukuryota, Motatoa, "Borlata, Crimiata, Vortobrata, Eutoboostumi,
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                                                                    15-JUL-1948 (Re) ^{-3.6} Last annotation update) MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).
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N-LINKED (GLCNAC. ) (POTENTIAL).

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Best Local Similarity
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INTERPRO: IPROUD276; ...
INTERPRO: IPROUD276; ...
PEAM; PEO0001: 7tm_1; 1.

PPAM; PEO0001: 7tm_1; 1.

PPAM; PEO0001: 7tm_1; 1.

PPAM; PEO0027: MELATONINA

PPAM; PEO027: MELATONINA

PPAM; PEO027: G_PROTEIN_FECEP_F1_1; 1.

PROSITE: PEO027: G_PROTEIN_FECEP_F1_2; 1.

PROSITE: FEO006: G_PROTEIN_FECEP_F1_2; 1.

G_PROTEIN COUPLED TRANSMEMBRADE: Glycoprotein.

G_PROTEIN_COUPLED TRANSMEMBRADE: Glycoprotein.

G_PROTEIN_COUPLED TRANSMEMBRADE: Glycoprotein.
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-(1 SUBCELLULAF LOCATION: INTEGRAL MEMBRANE PROTEIN FOR THE SPECIAL IN THE FRAIN, MORE PRECISELY IN THE FALS AND THE SUPPRACHIASMATIC NUCLEUS.
-(1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Reppert S M , Weaver D R , Ebisawa I .;
"Closing and characterization of a mammalian melatonin receptor that
                                                                                                                                                                                                                                                                            САРБОНУГ
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                                             MUSINGSALENASÓF---VLEGIGARESWLASALAGVILTETTVVDTIGNLLVILSVYRNKK 57
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  RESULT 3
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PRINTS: PRO0857; MELATONINR.

PRINTS: PRO1149: MELATONINAR.

PROSITE PRO0237: G_PECTEIN_PECEP_F1_1: 1.

R PROSITE: FSS0225: G_PECTEIN_RECEP_F1_2: 1.

R PROSITE: FSS0226: G_PECTEIN_RECEP_F1_2: 1.

R C-protein coupled receptor: Transmembrane: Glycoprotein.

R C-protein coupled receptor: Transmembrane: Glycoprotein.

TRANSMEM 3 2 1 (POTENTIAL).

TRANSMEM 3 5 1 (POTENTIAL).

TRANSMEM 3 66 CYTOPLASMIC (POTENTIAL).

TRANSMEM 67 87 2 (POTENTIAL).

TRANSMEM 88 105 EXTRACELLULAR (POTENTIAL).

TRANSMEM 106 126 3 (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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ROCA A.L., GodSon C., Weaver D.P. Peppert S.M.:

"Structure, characterization, and expression of the gene encoding the mouse Mella melatonin receptor.";

mouse Mella melatonin receptor.";

Endocrinology 137:3469-3477(1996).

Endocrinology 137:3469-3477(1996).

THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE GOF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE GOFOTELS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Richnformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Sce http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTNR1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ML1A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia: Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 LNONFPOEYKRILVSLETAKMOEVDSSNDPADKIKOKPAPLIANNNLIKVDSV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 INQNERKEYRRIIVSLCTARVEFVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 VTMEVVEVLFAICWAPLNFIGLIVASDPATMAPRIPEWLFVASYYMAYENSCLNAIIYGL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 VTMFVVFVLFAICWAPLNFIGLAVASDPASMVFKIPEWLFVASYYMAYFNSCLNAIIYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96290986; PubMed-8754776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       GCRDB: GCR_1650: -.
MGD: MGI:102967: MTNP1A
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                                                                                                                                                                                                                                            PFAM; PF00001;
                                                                                                                                                                                                                                                                               INTERPRO: IPR000025: -
                                                                                                                                                                                                                                                                                                                                                                        EMBL: U52222; AAB08755.1; -.
                                                                                                                                                                                                                                                               NIERPRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITGIAINRYCYICHSLKYDKLYSSKNSLCYVLLIW..LTLAAVLPNLRAGTIQYDPRIYSC
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                                                                                                                                                                                                                                            7tm_1;
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                        298 LNONFRKEYRRIIVSLCTARVFFVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 350
                                                                             238 VIMEVVEVLFAICWAPLNEIGLAVASDPASMVPRIFEWLFVASYYMAYENSCLNAIIYGL
301 LNQNFRKEYKKIIVSLCTAKMFFVESSNEEADKIKCKPSPLIPNNNLIKVDSV 353
                                                                                                                                                                                                          61 LRNSGNIFVVSLAVADLVVAVYPYPLVLTSILNNGWNLGYLHCQVSAFLMGLSVIGSIFN
                                                                                                                                                                                                                                    58 LRNAGNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFN 117
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                       1 MOGNGSALPNASOPVL---RGDGARPSWLASALACVLIFTIVVDILGNLLVILSVYPNKK 57
                                                                                                                                                                                                                                                               1 MKGNVSELLNATQQAPGGGEGGRPRPSWLASTLAFILIFTIVVDILGNLLVILSVYRNKK 60
                                                    VTMEVVEVLEAICWAPLNLIGLIVASDPATMVPRIPEWLEVASYYLAYENSCLNAIIYGL
                                                                                                     TETQSVSSAYT1AVVVFHFIVPMIIVIFCYLR1WVLVLUVR##VKPUNKFKLKFQDFRNF
                                                                                                                              TFAQSVSSAYTIAVVVEHELVPMIIVIFCYLRIWILVLQVBQRVKPDPKPKI.KPQDFRNF 237
                                                                                                                                                          ITGIAMNRYCYICHSLKYDKIYSNKNSLCYVFLIMMLTLIAIMPNLQTGTLQYDPRIYSC
                                                                                                                                                                                                                                                                                                                    297;
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                     353 AA;
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146
191
212
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                                                                                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                                                                               86.5%; Score 1570.5; DB 1; 84.1%; Pred. No. 9.2e-85;
                                                                                                                                                                                                                                                                                                                                                                                       39837 MW;
                                                                                                                                                                                                                                                                                                                      28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

N-LINKED (GLONAC...) (POTENTIAL).

N-LINKED (GLONAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
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A GOOD COORDINATE OF COORDINAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MELATONIN FECEPTOR TYPE 1A (MEL-1A-R) (CKA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P49285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken)
Eukaryota, Metazoa; Chc
                                                                               THIS RECEPTOR IS MEDIATED BY PERIUSSIS TOXIN SENSITIVE G PROTEINS THIS RECEPTOR IS MEDIATED BY PERIUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1. TISSUE SPECIFICITY: EXPRESSED IN OPTIC TECTUM AND RETINA, LESS IN NEOSTRIATUM, HYPOTHALAMUS AND THALAMUS.

1. RECEPTORS.

1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Melatonin receptors are for the birds, molecular analysis of two receptor subtypes differentially expressed in chick brain."; Neuron 15:1003-1015(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ML1A_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves;
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reppert S.M., Weaver D.R., Cassone V.M., Godson C.,
Kolakowski L.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Best Local :
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PRAM: PP00001: 7tm_1: 1.

PRINTS: PP00237: GPCRPHODOPSN.

PRINTS: PP00457: MELATONINA.

PRINTS: PR01149: MELATONINA.

PRINTS: PR01149: MELATONINA.

PROSITE: PS00237: G_PROTEIN_RECEP_F1_1: 1.

PROSITE: PS00237: G_PROTEIN_RECEP_F1_2: 1.

PROSITE: PS00237: G_PROTEIN_RECEP_F1_1: 1.

PROSITE: PS00252: G_PROTEIN_RECEP_F1_1: 1.

PS00252: G_PROTEIN_RECEP_F1_1: 1.

PS00252: G_PROTEIN_RECEP_F1_1: 1.

PS00252: G_PROTEIN_RECEP_F1_1: 1.

PS00252: G_PROTEIN_RECEP_F1_1: 1.

PS00252: G_PROTEIN_RECEP_F1_1: 1.

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PS00252: G_PROTEIN_RECEP_F1_1: 1.

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PS00252: 
MILIA_ HEEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U31820; AAA92498.1; GCRDB; GCR_1081; -.
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                                                                                                                                            POT REYEKTAVSECTAKAEEGUSSNUAADKIRSKESELIINNNOVKADSA 353
                                                                                                                                                                                                                                                                                                                                      187
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                                                                                                                                                                                         <04 KEYPELIVELCTARVEEVDEENDVADRVKWKESPLMINNNVVKVDSV 350</p>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 TEVVSLAVADLVVATYPYPLVLMSTENNGWNLGYLHCQVSGELMGLSVTGSTENTTGTAT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 NGSALPNASOPVI FOLMAPPSWLASALAGVLIFTIVVEILGNELVILSVYFNFKERNAGN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGTVLPR--DPPAEGSPERPPWYTSTLATILIETIVVDLLGNLLVILSVYENKKLRNAGN 55
                                                                                                                                                                                                                                        FYLFAYCWAPUNEIGLAYAYDEETIIEKIFEWLEYSSYYMAYENSCUNAIIYGUUNONEE
                                                                                                                                                                                                                                                                                    EVLEATOW&FLNETGLAVASOFASMVFFTFEWLFVASYYMAYFNSGLNATIYGLLNUNFR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRYCYTCHS: KYDKI YSSKNSI CYVILLIMLI TLAAVEPNERAGTI QYDPRIYSCI FAQSV 180
                                                                                                                                                                                                                                                                                                                                   SSAYTIAVVEEHEILEIAIVTYCYLEIWII VIQVERPVKPDNNPRLKPHDEENEVTMEVV
                                                                                                                                                                                                                                                                                                                                                                                SSAYTIAVVVEHELVEMITVIEGATIEMITATGARGRVKEDEKEKEGDEKNEVTMEVV 243
                                                                                                                                                                                                                                                                                                                                                                                                                            NRYTYICHSLKYEKLYSEKNSLCYVGLIWVLIVVAIVPNLFVGSLQYEPRIYSCIFAQSV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEAAL TVITATISTISTISTEMISTSTÄGHTANTANNENHAASTINTAAATTAATATATAT
  045608
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144542175
                        STANCARDS
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80.4%;
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5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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CYTOPLASMIC (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1509, DB
Fred. No. 3.3e-8
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GUGNAC) (POTENITAL)
N-LINKED (GLONAC) (POTENITAL)
- UBFU7807F1AF191D GF054
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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CYTOPLASMIC (
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EXTRACELLULAR (POTENTIAL)
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                        ASS AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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01-FER-1996 (Rel. 33
01-FER-1996 (Rel 33
01-0CT-2000 (Rel 40
MELATONIN RECEPTOR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U14109; AP
EMBL; AF045219;
HSSP; P29274; IN
                                                                  DOMAIN
DISULFID
                                                                                                                                                                                   TFANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PPOT entry is copyright It is produced through a collaboration between the Swiss Institute of Rioinformatics and the EMBL outstation the European Hoinformatics Histitute There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this stipperent is not through the switch according to the supperent is not the soul transport by and for commercial outside and the supperent appropriate the supperent is not transport by and for commercial or send an email to licenseeisb-sib.oh).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrett F. Commay S. Juckers R. Strusberg A.D.,

Barrett F. Commattre B. Delagrange P. Morgan P.J.;

Guardiola-Lemattre B. Delagrange P. Morgan P.J.;

"Cloning and functional analysis of a polymorphic variant of the owine

Mel la melatonin receptor."

Ricchim. Biophys. Acta 1356-294-307(1947)

FUNCTION. HIGH AFFINITY PECEFFORE FOR MELATONIN. LIKELY TO MEDIATES

THE REPRICUCITY AND CINCADIAN ACTIONS OF MELATONIN. THE ACTIVITY

OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G

OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G

PROTEINS THAT INHIBITS ADENVIATE CYCLASE ACTIVITY

OF STRUCTULAR FORMATION. INFERGRAL MEMBRANE PROTEIN.

THE SIMILARITY: HELONGS TO FAMILY 1 OF G-PROTEIN COURSED RECEPTORS.
     VARIANT
                                                                                                                                                                                                                                                                                            PRINTITE: PRANTENT: G.PROTEIN_PROCEP_F1_1; 1.

PROSITE: FSS0262; G.PROTEIN_PROCEP_E1_2; 1.

G-protein coupled receptor: Transmemblane: Glycoprotein: Pulymorphism.

DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).

TRANSMEM 46 66 I (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                PFAM: PF00001; 7tm_1; 1.
PRINTS: PR00857: MELATONINE.
PRINTS: PR01149: MELATONINIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                GCPDB: GCP_1583; -
INTEPPPO: IPRO00025; -.
INTEPPPO: IPRO00276; -.
INTEPPPO: IPRO02278; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PITUITARY PARS TUBERALIS;
MEDLINE=95033233; PubMed=7946354;
MEDLINE=95033233; PubMed=7946354;
Meppert S M., Weaver D R., Ebisawa T.;
"Clouding and characterization of a mammalian melatonin receptor that mediates reproductive and circadian responses.";
Neuron 13:1177-1185(1994).
                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97337902: PubMed=9194573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metaroa: Chordata: Oraniata: Vertebrata: Futeleostomi:
Mammalia: Euthoria: Cotartiodactyla: Fuminantia: Puccra- Boroldea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
                                   CARROHYD
                                                   CAPBOHYD
                                                                                                                      DOMAIN
                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                     PANEMEM
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33, Last sequence update)
40, Last annotation update)
6 IYPE ia (MEL-iA-k).
     EXÍMACECLULAÉ (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (SICHAC) (POT
N-LINKED (SICHAC) (POT
N-LINKED (SICHAC) (POT
N-LINKED (SICHAC) (POT
N-LINKED (SICHAC)).
N-> D (IN MEL 1A(BETA)).
N-> R (IN MEL 1A(BETA)).
                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (PUTENTIAL).

EXTRACETIMIAR (POTENTIAL).

5 (POTENTIAL).
                                                                                                                                                                                                                                                                  CYTOPLASMIC
2 (FOTENTIAL
                                                                                                                                   CYTOPLASMIC
5 (POTENTIAL
                                                                                                                                     (FUTENTIAL)
                                                                                                                                                                                                                                                                  (FOIENTIAL)
   D (IN MEL la(BETA)).
R (IN MEL la(BETA)).
                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                   ) (FOTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHICK
                                                 use by non-profit institute. There are no restrictions on its modified and this statement is not removed this content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MELATONIN RECEPTOR TYPE 1C (MEL-1C-R) (CKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota: Metazoa: Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P49288
                                                                                                                                                                                                                                                                                                                                                                                                   "Melatonin receptors are for the birds: molecular analysis of two receptor subtypes differentially expressed in chick brain.";
Neuron 15:1003-1015(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reppert S.M., Weaver D.R., Cassone V M., Godson C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96073557; PubMed=7576645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 LNCNFPKEYPPIIVSLCTARVFFVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 VTMFVVFVLFAICWAPLNFIGLVVASDPASMAPRIPEWLFVASYYMAYFNSCLNAIIYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 VIMEVVEVLEAICWAPLNEIGLAVASDPASMVPFIPEWLFVASYYMAYFNSCLNAIIYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 TFTQSV$SAYTIAVVVFHFIVPMLVVVFCYLRIWALVLQVRWKVKPDNKPKLKPQDFRNF
INTERPRO:
                         GCRDB:
                                        EMBL: U31821:
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                                                                                                                                                                                                                                                                               PINCTION: HICH AFFINITY RECEPTOR FOR MELATONIN. THE ACTIVITY OF FORTIST THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENVLATE CYCLASE ACTIVITY (BY SIMILARITY). SUBCELLULAR LOCATION: UNTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN OPTIC TECTUM, NEOSTRIATUM.
HYPOTHALAMUS, THALAMUS AND PINEAL GLAND, LESS IN CEREBELLUM AND
                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO FAMILY 1 OF G-PPOTEIN COUPLED PECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRNAGNVFVVSLAVADLLVAVYPYPLALASIVNNGWSLSSLHCQLSGFLMGLSVIGSVFS 133
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    GCR_1080
30: IPR000025: -.
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                                        AAA92499.1; -
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ID MLIC_XENLA

AC P49219;

AC P49219;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Cast sequence update)

DT 15-JUL-1996 (Rel. 36, Last annotation update)

DT 15-JUL-1996 (Rel. 36, Last annotation update)

DE MELATONIN RECEPTOR TYPE 17 (MEL-10-R).

DE MELATONIN RECEPTOR TYPE 17 (MEL-10-R).

CS Xenopus laevis (African clawed frog).
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RP RC
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FRUSITE: PS50262; G_PROTEIN_PECEP_F1_2: 1
G-protein coupled receptor: Transmembrane;
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INTERPRO; IPR002279; -.
PFAM; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS: PR00857; MELATONINR.
PRINTS: PR01150; MELATONIN1CR.
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                                                                                                                                     Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae
                                                                                                                                                                    Eukaryota, Metazoa, Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 FVVFVLFAVCWGPLNFIGLAVSINPSKVQPHIPEWLFVLSYFMAYFNSCLNAVIYGLLNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 QTVSTSYTITVVVVHFIVPLSIVTECYLRIWILVIQVKHRVPCCCKOKIRAADIRNELTM 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 NFRKEYKPILLMIRTPRLLEIDVSKGGTEGLKSKPSPAVTNNNQAEI 344
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MEDLINE-94286591; PubMed=7517042;

TISSUE=DERMAL MELANOPHORES;

SEQUENCE FROM N.A.

Xenopodinae;

Xenopus

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FRINTS: PF000857: MELATONINDP

FRINTS: FR01150: MELATONINDP

FROSITE: PS00237: G_PROTEIN_BECEP_F1_1: 1.

FROSITE: PS00236: G_PROTEIN_BECEP_F1_2: 1.

FROSITE: PS00262: G_PROTEIN_BECEP_F1_1: 1.

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Proc. Natl Acad Sci. U.S.A. 91:6133-6137(1994).

PROC. TOUR HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATE THE POTENT EFFECTS OF MELATONIN ON PROMENT AGGREGATION IN MELANOPHORES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY
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or send in remail to licenserisb-sib.ch).
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"Expression eleming of a high-affinity melatonin receptor from
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RESULT 8
ML1A_BOVIN
ID ML1A_BOVIN
AC 002769
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Hoinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not ramewed in sage by and for commercial entities requires a license agreement (See hittp://www.isb-sib.ch/ancounce/or-send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Womanck J.E. Barendse W. Crawford A.M., Notter D.R., Rothschild M.F.;
                                                                                                                                                                                                   PROSITE: PS00237: G_PROTEIN_RECEP_F1_1; 1.

PPOSITE: PS50262: G_PROTEIN_RECEP_F1_2; 1.

O_Protein coupled receptor: Transmembrane:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last segment update)
15-JUL-1998 (Rel. 36, Last annotation update)
MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (FRAGMENT)
SEQUENCE
                                                                   DOMAIN
                                                                                                                                                               TRANSMEM
                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                        EMPL: U73327; AAC48725 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mamm Genome Kikhi-370(1497).

-1: FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN, LIKELY TO MEDIATE, THE PEPFOCUCTIVE AND CIMOACIAN ACTIONS OF MELATONIN, THE ACTIVITY OF THIS PECFOCO IS MEDIATED BY PERFUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

-1: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=HYPOTHALAMUS, AND PITUITARY;
MEDLINE=97252109; PubMed=9107687;
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                                        DOMAIN
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                                                                                                                                                                                                                                              PFAM: PF00001; 7tm_1;
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                                                                                                                                                                                                                                                              INTERPRO
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                                       43
107
128
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29370 MW;
                 BY SIMILARITY.
                                       7 (POTENTIAL)
CYTOPLASMIC (
                                                                               CYTOPLASMIC
6 (POTENTIA:
                                                                                                          EXTRACELLULAR (FOTENTIAL) 5 (POTENTIAL).
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                                                                                             (POTENTIAL).
                                                                   (POTENTIAL)
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Query Match Best Local Similarity Matches 217: Conserv

Conservative

100

Mismatches

Pred. No. 5.5e-62;

Length 257;

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Gaps

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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MELATONIN RECEPTOR TYPE 1B (MEL-1B-R) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria, Aves:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LVVIECYLRIWALVEGVEWRVKFDNKFKLKEGDTENEVTMEVVEVLEAIGWAPUNEIGLV 180
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu F., Yuan H., Sugamori K.S., Hamadanizadeh A., Lee F.J.S.,
Pang S F, Brown G.M., Fristupa Z.B., Niznik H R :
"Molecular and functional characterization of a partial cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96063731; FubMed-7589552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
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                                                                                                                                                                                                                                                                               or send an email to licensewisb-sib.ch)
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 TRANSMEM
DOMAIN
                                                                                                                                              PFAM: PF00001: 7tm_1: 1
prosite: PS00237: G_PROTEIN_PFCEP_F1_1: 1
PROSITE: PS50252: G_PROTEIN_PFCEP_F1_2: 1
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                                                                                                                                  G-protein
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                                                                 C-MAIN
                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel chicken brain melatonin receptor.":
:BS_Lett. 374:273-278(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION. HIGH AFFINITY RECEPTOR FOR MELATONIN, THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SINILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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                                                                                                                                  coupled receptor:
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Neognathae: Galliformes: Phasianidae, Fhasiani
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                                                                                                                                     Transmembrane; Glycoprotein
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     3 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                     CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                       EXTRACELLILAR (POTENTIAL)
3 (POTENTIAL)
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DOMAIN
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01-FEB-1996 (Rel. 3), Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation updat
KELATONIN PECEPTOR TYPE 1B (MEL-1B-R).
                                                     Genetic polymorphisms of human melatonin 1b receptor gene in circadian rhythm sleep disorders and controls."

Neurose's 15tt 280-29-32(2000).

Neurose's 15tt 280-29-32(2000).

THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY PROFESSED IN PERTUSALS IOXIN SENSITIVE GOF THIS RECEPTOR IS MEDIATED BY PERTUSALS IOXIN SENSITIVE GOF THIS RECEPTOR IS MEDIATED BY PERTUSALS IOXIN SENSITIVE GOF THIS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

SUBGELLUAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reppert S.M., Godson C., Mahle C.D., Weaver D.R., Slaugenhaupt S.A., Gusella J.F.; Slaugenhaupt S.A., Gusella J.F.; "Molecular characterization of a second melatonin receptor expressed in human retina and brain: the Wellb melatonin receptor."; proc. Natl. Acad. Sci. U.S.A. 92:8734-8738(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=96004613; PubMed=7568007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Crdillata, Velcebiata, Homo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ML1B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 SVSSAYTIAVVVEHELVPMIIVIFCYLRIWILVLQVPQEVKPDPKPKLKPQDEENFVTMF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AINRYCYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLRAGTLQYDRHYSCTFAO 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 FRKEYRRIIVSLCTARVFFVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VVFVIFAFCWAPLNFIGLAVAINPSEMAPKVPEWLFIISYFMAYFNSCLNAIIYGLLNQN
                                                                                                                                                                                                                                                                                                                                         Kudo Y., Iwase T., Sugishita M., Jodoi T., Ikeda M., Ozeki Y.,
Watanabe T., Sekimoto M., Katoh M., Yamada N., Toyoshima R., Ukawa
Takahashi K., Yamauchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GNIFYVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS G
MEDLINE=20159877; PubMed=10596804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Nati. Acad. Sci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TASSYYTIAVVVIHFIVPITVVSFCYLRIWVLVLQVRRRVKSETKPRLKPSDFENFLTMF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AINRYCYICHSFAYDKVYSCWNTMLYVSLIWVLTVIATVPNFFVGSLKYDPRIYSCTFVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIIYGLLNON 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRNEYKÉTLMSLWMPÄLFFYUTSKGGTDGQKSKÉSFALNNNUQMKTETT. 280
   HIPPOCAMPUS. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                         T., Uchiyama M., Kajimura N., Kamei Y., Iwase T., Suqishita M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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69.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND VARIANTS GLU-24 AND PHE-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation update) (MEL-1B-R).
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6 (POTENTIAL).
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibui K., Kim K.,
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PFINITS: PP00277: GPCFFHODOPSN.
PRINTS: PP00857: MELAFONINE
PROSITE: PS00277: G_PPOTEIN_PECEP_F1_1: 1
PP0SITE: PS00277: G_PPOTEIN_PECEP_F1_2: 1.
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PFAM; PF0uvul; 7tm_l; 1
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316 RREYKRILLALWNPFHCIQDASKGSHAEGLQSPAP 350
                                                                                          24 F VEVLEATOWAPLNETGLAVASDPASMVPRTPEWLEVASYYMAYENSCLNATTYGLLNONE
                              333 KKEYRRIIVSLCTARVFFVDSSNDVADRVKWKPSP 337
                                                                                                                                                  183 VSSAYTIAVVVYSHELVEMIIVIFGYLEIWILVIQVEQPVKFDPKEKCKEQDERNEVTMEV 242
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                               TO CHERCYTCHELMYDKLYSSKNSTCMATTIMETETAAMTENTBAGTLOMDPBIMSCTFAQS 182
                                                                                                                                                                                                                                              76 NLFLVSLALADLVVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIA 135
                                                                                                                                                                                                                                                                         63 NIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIA 122
                                                                                                                                                                                                                                                                                                        24 GAGSARPSPT------PPPPPWVAPALSAVLIVTTAVDVVGNLIVILSVLPNPKIPNAG 75
                                                                                                                                                                                                                                                                                                                                     3 GNGSALPNASQFYLRGDGARPSWLASALACYLIFTIYVDILGNLLYILSYYRNKKLRNAG 62
                                                           VEVIFAICWAPLNCIGLAVAINFOEMAFQIPEGLEVTSYLLAYENSCLNAIVYGLLNONF
                                                                                                                       ASTOYTAAVVVIHELLPIAVVSFCYLPIWVLVLQAPPKAKPESPLCLKPSDLRSFLTMFV
                                                                                                                                                                                  INRYCYICHSMAYHEIYERWHTFLHICLIWLLIVVALLPNFFVGSLEYDPRIYSCIFIQI
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AB033598; BAA92315.1;
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135
175
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4 (POTENTIAL).
4 (POTENT:
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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, EBCH786492579111 CRC64
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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RESULT 11
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Q13585;
G1-NOV-1997 (Re)
G1-NOV-1997 (Re)
30-MAY-2000 (Re)
                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial continues requires a library agreement (see http://www.isbesib.eb/dimension/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                          G-protein coupled receptor;
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PRO5SITE; PS00237; G_PROTFIN_RECEP_F1_1; 1.
PRUSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                 GCRDB;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota, Metazoa,
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                                                                                              SEQUENCE
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15 GCKLPQPEYP------PA-LIIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNI 65
                                                    Local
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                     5 GSALFNASSFYLEGESARFSWLASALASVLIFTIVVUILGNILVILSVYPNKKLRNAGNI 64
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                                         al Similarity
161; Conserv
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0001; 7tm_1
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                                                                                                <13 AA
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35, Last sequence
39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR (H9).
                                         49.1%; Score 891.5; DB 1;
49.5%; pred. No. 2.7e-45;
zative 71; Mismatches 82;
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                                                                                                                             6 (POTENTIAL).
EXTRACELLULAR
7 (POTENTIAL).
CYTOPLASMIC (P
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5 (POTENTTAL)
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                                                              DB 1; Length 613;
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Q20558; Q46624;
01-NOV-1997 (Rel. 3
15-DEC-1998 (Rel. 3
15-JUL-1999 (Rel. 3
                         INTERERO, 1880.

PEAM, PEOCODI, 7tm_1, 1.

PEAM, PEOCODI, 7tm_1, 1.

PROSITE, PSC0237 G_PROTEIN_RECEP_F1_1 1

PROSITE, FSC0262 G_PROTEIN_RECEP_F1_2 1.

PROSITE, FS50262 G_PROTEIN_RECEP_E1_2 1.

PROSITE, FS50262 G_PROTEIN_RECEP_E1_2 1.

PROSITE, FS50262 G_PROTEIN_RECEP_E1_2 1.

PROTEIN_RECEP_E1_2 1
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHEEP
                                                                                                                                                                                                                                                                                              EMBL; AE047829; AACC4275.1; ... EMBL; U50201; AAC48609.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 128-245 FECM N.A. MEDLINE=96228068; PubMed=8647286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The ovine melatonin related receptor, cloning distribution and binding studies.";
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                                                                                                                                                                                                                                                                                                                                                                       antities requires a linense agreement (Sae http://www.isb-sib-ch/Announne/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
     TRANSMEM
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                                                                                                                                                                                                             INTERPRO, IPROCO276,
INTERPRO, IPROC2280,
PEAM, PECCOCI, 7tm_1.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
MELATONIN-RELATED RECEPTOR (H9).
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                                                                          -!- FUNCTION: DOES NOT BIND MELATONIN.
-!- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY. BELONGS TO FAMILY 1 OF G-PROTEIN COUPLEY PETERTORS.
                                                                                                                                                                                                     Gubitz A.K., Peppert S.M.;
"Assignment of the melatonin-related receptor to human chromosome
                                                                                                                                                                                                                                                            MEDLINE=99134305; PubMed=9933574;
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between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation -
                                                                                                                                                                (GFR50) and mouse chromosomo X (GFr50) Genomics 55-248-251(1999)
                                                                                                                                                                                                                                                                                                                                   Mammalia;
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P -> 1 '''
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L -> M (IN REF. 2).
ARD -> D (IN REF 2).
; E2CAlCllFFE7DEF8 CRC64;
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CYTOPLASMIC (
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5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
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3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                   Craniata, Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583
                                                                                                                                                                                                                                                                                                                                                          Vertebrata,
         There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   Muridae;
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         restrictions on
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                                                                                                                 RAT
                               Ol-FER-1996 (Rel. 33, Created)
Ol-FER-1996 (Rel. 33, Last sequence update)
Ol-FER-1996 (Rel. 33, Last annotation update)
MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DISULFID
 Bukaryota:
           Rattus norvegicus (Rat)
                          MTNRIA
                                                                                       P49218;
                                                                                                     MI.IA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled receptor; DOMAIN 1 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                       EYRRIIVSLCTARVFFVDSSNDVADRVKWKPSPL 338
                                                                                                                                                                                                                LLFAVCWCFVNVLTVLVAVIPKEMAGKIPNWLYLAAYCIAYFNSCLNAIIYGILNESFRR
                                                                                                                                                                                                                                                               PAFTVTIVCIHFVLPLIIVGYCYTKIWIKVLAARD--PAGQNPDNQFAEVRNFLTMFVIF
                                                                                                                                                                                                                                     VLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIIYGLLNQNFRK
                                                                                                                                                                                                                                                                                      SAYTIAVVVFHELVPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPQDFRNFVTMFVVF
                                                                                                                                                                                                                                                                                                              RYCYICHSLQYKRIFSLRNTCIYLVVTWVMTVLAVLPNMYIGTIEYDPRTYTCIFNYVNN
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                                                                                                                                                                                                                                                                                                                                                                FVASLSVADMLVAIYPYPLMLYAMSVGGWDLSQLQCQMVGLVTGLSVVGSIFNITAIAIN
                                                                                                                                                                                                                                                                                                                                                                                      FVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIAIN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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PS00237; G_PROTEIN_RECEP_F1_1; 1

PS50262; G_PROTEIN_RECEP_F1_2; 1
Metazoa, Chordata, Craniata, Vertebruta, Euteleostami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002280;
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                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 862.5;
Fred. No 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
; D7135C0C4B3A2426 CPC64.
                                                                                                 PRT;
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RESULT 1
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                                                                                                                                                                                           ML1A_PIG
002781;
TISSUE=HYPOTHALAMUS, AND PITUITARY; MEDLINE+97262109; FubMed**9107687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-protein
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                SEQUENCE FROM N.A.
                                                                            Eukaryota;
                                                                                             Sus scrofa (Pig).
                                                                                                              MTNR1A
                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MELATONIN RECEPTOP TYPE 1A (MEL-1A-P) (FEAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Tage by and for commercial
                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U14409; AAA57191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.ish-sib ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuron 13:1177-1185(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mediates reproductive and circadian responses."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-HYPOTHALAMUS, AND PITUITARY; MEDLINE-95033233; FubMed-7946354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reppert S.M., Weaver D {\tt F} , Ebisawa T.; "Cloning and characterization of a mammalian melatonin receptor that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia, Eutheria, Rodentia, Schurcenathi, Muridae, Murinae; Rattus
                                                                                                                                                                                                                                                                                                                        247 FAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYY 282
                                                                                                                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 CYICHSLKYDKLYSSKNSLCYVILITHILTLAAVLPNLRAGTLQYDPRIYSCTFAQSVSSA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thes 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO
                                                                                                                                                                                                                                                                                         121 FALCWAPLNFIGLIVASDPATMAPRIPEWLFVASYY 156
                                                                                                                                                                                                                                                                                                                                                       61 YTIALVVEHEVVPMIIVTECYLRIWILVLQVRRRVKPDSKPKLKPQDERNEVTMEVVEVL
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CYICHSEKYURIYSNKNSLCYVFLIWILILLAIMPNLQTGTLQYDPRIYSCIFTQSVSSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: AT LEAST IN THE BRAIN, MOPE PRECISELY IN THE PARS TURERALIS AND THE SUPRACHIASMATIC NUCLEUS.
SIMILARITY: RELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY OF THIS PECEPTOP IS MEDIATED BY PEPTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: HIGH AFFINITY PECEPTOR FOR MELATONIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                     YTIAVVVEHELVPMIIVIFCYLRIWILVLQVEQEVKPDRKPKLKPQDEENEVIMEVVEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '03001; 7tm_1; 1.

FS00237; G_PROTEIN_RECEP_F1_1; PARTIAL FS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
115
115
156
                                                                              Metazoa;
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                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
82
135
156
158
18214 MW,
                                                             Cetartiodactyla; Suina; Suidae;
                                                                              Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.4%;
87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 751; DB 1; Fred. No. 1.3e:37;
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                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                           154 AA
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                                                                              Eutelecstomi;
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Job time: 3256 sec
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib ch/announce/or send an email to license@isb-sib.ch).
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Womack J.E., Barendse W., Crawford A.M., Notter D.R.,
Rothschild M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mapping of the melatonin receptor la (MTNRIA) gene in pigs, sheep, and cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; Transmembrane; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS50262; G_PROTEIN_PECEP_F1_2; 1.
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                                                                                                                                                             121 LFAICWAPLNFIGLAVASDPASMAPRIPEWLFVA 154
                                                                                                                                                                                                                        246 LFAICWAPLNFIGLAVASDPASMVPRIPEWLFVA 279
                                                                                                                                                                                                                                                                                       61 AYTIAVVVEHELVPMVIVIFRYLRIWVLVLQIRWRAKPENNPRLKPQDFRNFVTMEVVFV 120
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SUBCELLULAR LOCATION: INTEGRAL MEMPRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                        1 YCYICHSLKYDRWYSNRNSLCCVFLICVLTLVAIVPNLCMGTLQYDPRIYSCTFAQSVSS 60
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3A - *FESWENSALACVLIE ! I VYOT	*: Soure 1499; DB 6; T. *: Pred. No. 4.8e-107; 27; Mismatches 25;	gl94573; ckers R., Strosberg A.D., layrange P., Morgan P.J.; nalysis of a polymorphic va 56:299-307(1997). 56:299-307(1997). 1; regan P.J.; hu EMBL/GenBank/DUBJ databa li; rNR. RNIAR. RNIAR. ENL BA71B5DFTFD398FC CFC(9 MW; BA71B5DFTFD398FC CFC(pRT; 366 AA. (Created) (Last sequence update) (Last annotation update) (Last annotation update) (Last annotation update) (Last annotation update)	C57463 C57463 C9W534 C9WCZ3 C9CZ3 C75194 C9U721 C9U721 C9U721 C9U717 C9U717 C9TTC4 C9TTC4 C9TTC4 C9TTC2 C9TTC3 C9T
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101-MAY-1999 (TrEMBLrel. 10, Created)
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13-00 hamster). Workebrata:
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PRINTS: PR011149: MELATONIN1AB
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Eukaryeta: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Cricetinae;
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42 VSLAAADLVVAIYFYFLVLTSIENNGWNLGYLHCQISAFLMGLSVIGSIENITGIAINRY 121
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INTERPRO: IPRO02016: -.
INTERPRO: ITPO02278: -.
INTERPRO: TTPO02278: -.
PEAM: PF00001: 7tm_1: 1.
PPINTS: PP00237: GPCBPHONOPSN.
PPINTS: PP00357: MELATONINE.
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"Expression of rainbow trout melatonin Receptor.";
submitted (JUN-1940) to the EMELOBERS, [66: databases, EMBL, AD15652; AMFORDELL; -.
INTERPRO: IPP00025; -.
INTERPRO: IPP000276; -.
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01-MAY-ZUOU (TEMBLEEL. 13, last sequence update)
01-GT-ZOOO (TEMBLEEL. 15, Last sequence update)
01-GCT-ZOOO (TEMBLEEL. 15, Last sequence update)
MELATONIN RECEPTOR MELLA
GROOTYNICHUS Tykiss (Painbow trout) (Salmo gairdneri).
GROOTYNICHUS Tykiss (Painbow trout) (Salmo gairdneri).
Eukaryota, Melanoa, Chorlata, Oraniata, Variabrata, Estivitustomi).
Actinopterygii, Neypterygii, Teinostel, Estelesstei,
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Wiel_Taxite9822;
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Pred. No. 5.4e-101;
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Best Local
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01-MAY-1997 (TrEMBLiel
01-007-2000 (TrEMBLiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P., Morgan J.P., Guardiola B., Delagrange P., Marullo S., Strosberg A.D., Submitted (MAR-1997) to the EMBL /ConBank/DDBJ databases EMBL U57889; AAB48389.1: -
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X-nopus laevis (African clawed frog).
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INTERPRO: IPPN002279. ..
PEAM: PEN00001; 7'tm_1: 1.
PRINTS: PR000857: MELATONING.
PRINTS: PR01150; MELATONINGR.
PROSITE: PR00127: G_PROTESIN_PECFPTOP: UNKNOWN_1.
PROSITE: PS00227: G_PROTESIN_PECFPTOP: UNKNOWN_1.
SEQUENCE 354 AA; 39881 MW; BCF78D208F0C97A6
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   P87496;
01-MAY-1997 (TrEMBLrel. 03, Created)
                                    P87496
                                                                                                                                                                                                                                                                                     205 CYLRIWII VLOVBORVEPDPKPKI, KPODERNEVTMEVVFVLEAICWAPLNEIGLAVASDP 265
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                                                                                                                                                                                     271 FHVAPKIPEWLFVLSYFMAYFNSCLNAVIYGVLNQNFRKEYKRILMSLLTPRLLFLDTSR 330
                                                                                                                                                      226 DVADRVKWKPSPLMTNNN 343
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                                                                                                                                                                                                                                                                                                                                                                                                                        MSIFNNGWNLGYLHCOVSGFLMGLSVIGSIFNITGIAINRYCYICHSLKYDKLYSSKNSL 145
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                                                                                                                                                                                                                      ASMYPRIFEWLFVASYYMAYFNSCLNAIIYGLLNQNFRKEYRRIIVSLCTARVFFVDSSN 325
                                                                                                                                                                                                                                                       CYLRIWVLVIQVKHRVEQDEKQKLTQTDIBNELTMEVVEVLFAVCWAPLNEIGLAVAINP 270
                                                                                                                      GGTEGLKSKPSPAVINNN 348
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                                    PPELIMINARY.
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70.4%; Pred. No. 1
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MEL-1C(B) MELATONIN RECEPTOR.
Xenopus laevis (African clawed frog).
Eukaryota: Motazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa: Chordata: Mesobatrachia; Pipoidea; Pipidae;
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EMBL, U67882, AAB48392.1; -.
EMBL, U67881, AAB48392.1; -.
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PRINTS; PRO150; MELATONINICR.
PROSTTE, FSC0337; G_PPOTEIN_RECEPTOR; UNKNOWN_1.
SECUENCE 354 AA; 39931 MW; FD6FCZEBE336561D
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                                                                                                                                                                                                 oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                            Q9F133 FRELIMINARY; PRT; 152 AA G9F133; G9F133; O1-MAY-2000 (TrEMBLrel. 13, Created) O1-MAY-2000 (TrEMBLrel. 13, Last sequence update) O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Mazurais D., Brierley I , Anglade I., Michel D., Kah O., Williams L.M.;
                                                                                                                                                                                                                                                                                                                                           MELATONIN RECEPTOR (FRAGMENT).
                                                                     SEQUENCE FROM N.A. MEDLINE=99306591: PubMed=10379923:
                                                                                                                                                                       NCBI_TaxID=8022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 GGTEGLKSKPSPAVTNNN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 DVADRVKWKPSPLMTNNN 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 LHVAPKIPEWLFVLSYFMAYFNSCLNAVIYGLLNQNFRKEYKRILMSLWTPRLLFLDTSR 330
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                                                      Drew
                                                      Randail C., Bromage N.,
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Best Local :
                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                       Receptor.
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"Contral melatonic receptors in the rainbow trout: comparative distribution of ligand binding and gene expression."; J. Comp. Neurol. 409:813-924(1999).

EMRI: AF178548: AAD54384.1: -.
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    -uncorhynchus mykiss (Rainbow trout) (Salmo dairdheri).
    -uncorhynchus mykiss (Phoridata (Prandata) (Parrebrata) (Intelenstemi).
    -uncorhynchus (Phoridata) (Parrebrata) (Intelenstemi).
    -uncorhynchus (Protacanthopteryqii) (Salmeniformes) (Salmenidae) (Uncorhynchus).

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01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-007-2000 (TrEMBLrel, 15, Last annotation update)
MELATONIN RECEPTOR (EAGGMENT).
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PRINTS: PR00857: MELATONINR.
PRINTS: PR01149: MELATONIN1AR
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J. Comp. Neurol. 409:313-324(1999).
EMBL: AF178929; AAD51850.1; -.
INTERPRO; IPR0000225; -.
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEAM; PE00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99306591; PubMed-10379923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N'HI_TaxID-8022
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PFAM; PFODOO1:
                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PROOB57; MELATONINE
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127 CYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLKAGTLQYDPRIYSCTFAQSVSSA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 FAIRWAPINEIGLAVASDPASMVPRIPEWLFVASYYMAYFNS 288
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hes 117; Conserv
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                                                                                116:
                                                                         Similarity 71.6
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0001: 7tm_1: 1
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)001; 7tm_1;
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162
157 AA:
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                                                                                                                                                                                                                                                          161
161 AA;
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                                                                     35.5%; Score 644.5; DB 1
71.6%; Pred. No. 3 76-42;
vative 24; Mismatches 23
                                                                                                                                                                                                                                                          18860 MW; D3BA33C86512DAA3 CRC64
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Pred. No. 6e-44;
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                                                                                                                                              DB 13; Length
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Best Lucal :
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SECTENCE
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01-MAY 1999 (TrEMBLrel. 10, Created)
01-MAY 1999 (TrEMBLrel. 10, Last sequence update)
01-un-2000 (TrEMBLrel 14, Last annotation update)
ELATONIN PECEPTOP 1A (FPACHENT).
                                                          Rathus norvegious (Rat)
Eukaryota: Metacos: Chordata: Craniata: Vertebrata: I
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae:
                                                                                                                                                   09JLR8:
01-001-2000 (Iremblrel 15, Created)
01-007-2000 (Tremblrel 15, Last sequence update)
01-007-2000 (Tremblrel 15, Last annotation update)
mil melaTONIN RECEPTOR MEL-1B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elaysky N.E. Ernst C.W., Messer L.A., Rothschild M.F.; "Identification of Sequence Tagged Sites in the Asian Elephant (Elephas maximus) and the African Elephant (Lexedonta africana)."; Submitted (MAP-1947) to the EMEL/GenHank/DDRJ darabases.
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO: TRR000276; --
INTERPRO: TRR002278;
PFAM: PF00001; 7tm_1; 1.
PRINTS: PR00237: GPCPRHODOPSN.
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Mammaila: Buthotla: Profesoidea: Biephas/Idae: Elephas
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Eukaryota: Metazwa: Chotdata: Cranjata: Vertebiata, Eutoleustomi:
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129 AA
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Foirel V.J., F
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01-FEB-1997 (TrEMBLrel 02, Last sequence update)
01-GCT-2003 (TrEMBLrel 15, Last annotation update)
MEL-1B MELATONIN RECEPTOR (FRAGMENT).
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                                                                                                                                                                                                                                                             NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VFAICWAPLNCIGLAVAINPEAMALQIPEGLEVTSYFLAYFNSCLNAIVYGLLN 174
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                            Weaver D.R.
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                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                       7. P.A.M.
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NTERFRO IFROCEZES: -
PAM, PECCOCOL: 7tm_l:
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                                                                                                                                        TOK YOYLOHSILKYDKIVSSKNSLOYVILLIWILTLANVLPNLRAGTLQYDPRIYSOTFAOSVSS 185
                                                                                 195 AYTIAVVVEHELVƏMIIVIECYLRIMILVLÇVEQRVKPDRKPKLKPQDERNEVTMEVVEV 245
                          245 L 246
121 V 121
                                                     61 QYTAAVVAIHELLEMAVVSECYLRIWVLVLQAPEKAKATEKLELPESSLESSLIMSAVEV 120
                                                                                                             1 YCCICHSTTYHRVCSHWYTPIYISLVWLLTLVALVPNFFVGSLEYDPRIYSCTEIQTAST 60
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109; Conserv
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                                                                                                                                                                                                                                                                                        FR00857; MELATONINR
                                                                                                                                                                                       Similarity
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174 AA:
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(MAY-1996) to the EMBL/GenBank/DDBJ databases
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121 AA,
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19857 MW:
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                                                                                                                                                                                                                                                14063 MW; A237606802950BlC CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chordata.
                                                                                                                                                                                       21.3%. Score 387; DB 11; Length 121; 57 (%: Fred. No. 1.3e-22;
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SCORRESPONDED TO THE PROPERTY OF THE PROPERTY 
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RA Adams M.D. Celinker S.E. LIP.W. Hoskins R.A. Galle R.F.

RA Amanatidos P.G. Scheret S.E. LIP.W. Hoskins R.A. Galle R.F.

RA Sauthon G.G. Wortman J. P. Yandell M.D. Zhang W. Chen L.X.

RA Sauthon G.G. Wortman J. P. Yandell M.D. Zhang W. Chen L.X.

RA Sauthon G.G. Wortman J. P. Yandell M.D. Zhang W. Chen L.X.

RA Sauthon B.G. Wortman J. P. Yandell M.D. Zhang W. Chen L.X.

RA Abril J.F. Agbayani A. An H.-J. Andrews-Flankoch J. Esthery E.M.

RA Abril J.F. Agbayani A. An H.-J. Andrews-Flankoch J. Esthery E.M.

RA Abril J.F. Agbayani A. Baxendale J. Bayraktaroglu L. Beasley E.M.

RA Abril J.F. Agbayani A. Baxendale J. Bayraktaroglu L. Beasley E.M.

RA Beeson K.Y. Benos P.V. Borman b.P. Blandari C. Boishakov S.

RA Berson K.Y. Benos P. Borne H. Cadleu E. Cotter A. Chandra J.

RA Cherry J.M. Cawley S. Dahlke C. Davenport L.B. Davies P.

RA Cherry J.M. Cawley S. Dahlke C. Davenport L.B. Davies P.

RA Cherry J.M. Cawley S. Dahlke C. Davenport L.B. Davies P.

RA Dodson K. Doup L.E. Downes M. Dugan-Rocha S. Dunkov B.C. Bunkov B.
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C1-MAY-2000 (TrEMBLIEL: 13,
01-JUN-2000 (TrEMBLIEL: 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9W498
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Ephydroidea: Drosophilidae: Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthiopoda. Tracheata: Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29W498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-7227
                                                                                                                                                                                                                                                                        ELYBASE; reyucct
INTERPRO, IFROCOD76; 1.
PEAM; PEO0001; 7tm_1; 1.
PRINTS; FROCO27; GPCPPFOTEIN_PECEPTOR; 1.
PROSTITE: FSOCO27; G_PPOTEIN_PECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003435; AAF46059.1; FLYBASE; FBgn0029786; CG3171.
                                                                                                                                                                     Local Similarity
                                                                  27 ASALAGVLIFTIVVDILGNLLVILSVYRNKKLR-NAGNIFVVSLAVADLVVAIYPYPLVL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 PROTEIN.
32 AAISACVF---VTIGVLGNLITLLALLKSPTIREHATTAFVISLSISULLFCSFSLPLTA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                               Conservative
                                                                                                                                           18.8%; Score 341.5;
26.6%; Pr=3 No 1 26
ative 68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                           20-18
                                                                                                                                                                                                                        DB 5; Length 386;
                                                                                                                                                                 Indels
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                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 "Functional identification of the gene for Drosophila gustatory transduction of the sugar taste."

Debuttsquada Jassia Paridon-journeys
                                                                                                                                                                                                                                                                                                                                                          Dobutsudaka Kasshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIRAIN-Y(2), ON BW SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Y(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-00T-2000 (TIEMBLIEL 15, Created)
01-00T-2000 (TEMBLIEL 15, Last sequence update)
01-00T-2000 (TIEMBLIEL 15, Last annotation update)
TASTE RECEPTOR PROTEIN TRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIRAIN-Y(2), ON BW SP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nikajima S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2000) to the EMBL/GenBank/TOBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakajima S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CMUNE
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                  EMBL: AB042625; BAA96500.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular analysis of the expression of the prosophila tasto gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHOM2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sbutsugaku %seebi To::!s-!!5(lasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 LCYVILIWILTIAAVIPNI.PA--GTIQYDPRIYSCTFAQSVSSAYTIAVVVFHFLVPMII 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20% VIECYLRIWILVLQVRQPVKP-----
PS VREFQESWTFGTTLCKIFPVIFYGNVAVSLLSMVGITLNRYILIACHS-RYSQIYKPKFI 153
                                          46 MSTENNOWNLOYCHOOVSGELMGLSVIGSTENITGIAINRYCYI-CHSLKYDKLYSSKNS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 VREFQESWTFGTTLCKIFPVIFYGNVAVSILSMVGITLNRYILIAGHS-RYSQIYKPKFI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 MSTENNOWNLGYLHOOVSGELMGLSVIGSTENITGIAINRYCYT-CHSLKYDKLYSSKNS 144
                                                                                    AAISAMVF---VTIGVLGNLITLLALLKSPTIREHATTAFVISLSISDLLFCSFSLPLTA 94
                                                                                                                              ASALACVLIFTIVVDILGNLLVILSVYRNKKLR-NAGNIFVVSLAVADLVVAIYPYPLVL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNRNYRVAYYKIFALL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNONFRKEYRRIIVSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMMVTIFLCFLVCFLPL-MLANVVDDERNTSYP----WLHIIASVMAWASSVINPIIYAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTMFVVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIIYGL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUQULEVWAVSELLILEPILGIWGEMGI.DEATESCTILKKEGPSIKKTUFVIGEULPCUV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIVSYSTIYITVIHOKKKIENHONEQIAAAKGSSSSGGSSYMTTTCTEKAR---EDNELT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Deno K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beno K., Morita H., Isene K., Tsukahara Y., Mikani Y
                                                                                                                                                                                                                                                                                                                                                                                                                           ., Yamamoto K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ueno K
                                                                                                                                                                                                                                                                                           392 AA: 43843 MW; 41A580594798BFDA CRC54;
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto K
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                                                                                                                                                                                                                                                                                                                                                                                                                                              . Morita H., Obta M., Tsukabara Y., Nakajima S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Morita H., Ohta M., Tsukahara Y., Mikuni Y.,
                                                                                                                                                                                               18.8%; Score 341.5; DB 5; Length 392; 26.5%; Pred. No. 1.2e-18;
                                                                                                                                                                             68; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                   Constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachycera; Muscomorpha.
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                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                          guery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Multiplivity of neutropepto
subtype in the zebrafish.":
Ploabom Riaphys Pos Comm
Annal 276.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TIEMBLIEL, 07, Created)
01-AUG-1998 (TIEMBLIEL, 07, Last sequence update)
01-TUN-2000 (TIEMBLIEL 14, Last annotation updat
NEUPOFEFILE Y/FEFILE YY FECEFTOR YA.
                                                                                                                                                                                                                                                                                                                                SEMPLETINGE 1377 AA: AARROL MW; FREENARROTTERFERO TRO64;
                                                                                                                                                                                                                                                                                                                                                                    PEAM, PEO0001, 7tm.1; 1.
PEINTS: PROCERT: GROPPHONDEN.
PRINTS: PROCERT: GROPPHTIDEYP.
PROSETT: PS00237; G_PROTEIN_PECEPTOP: UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF037400; AAC41276.1; -. 2FIN; 2MB-GENE-990826-793; npyrya.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98095393; PubMed=9434780;
Ringvall M., Berglund M.M., Larhammar D.;
"Muitiplinity of protypeptide V receptors: cloping of a third distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subtype in the zebrafish.";
ENA Cell Biol. 16:1357-1363(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R Larhammar D.;
"Cloning and characterization of a novel neuropeptide Y receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinopteryvii: Neupteryvii: Teleustei: Bute
Cypriniformes: Cyprinidae: Pasborinae: Danio
NCBI_Taxiu=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metaroa: Chordata: Craniata: Vertebrata: Euteleostomi:
Actinopteryvii: Neopteryvii: ieleostei: Euteleostei: Ostariophysi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98068842; PubMed=9407007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPROGOGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
139 YSSKNSLCYVLLIMLITLAAVLENIKAGILQYDE-----KIYSCIE---AQSVSSA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 VMMVTIFLCFLVCFLPL-MLANVVDDERNTSYP----WLHIIASVMAWASSVINPIIYAA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 IIVSYSCIYITVLHQKKKIPNHONEQIAAAKGSSSSGGGSYMTTTCTRKAR---EDNRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 AIECATHIMITAIOANGAARD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 LCYVLLIWELTLAAVLPNLRA--GTLQYDPRIYSCTFAQSVSSAYTIAVVVFHFLVPMII 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 SNRNYRVAYYKIFALL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 LNQNFRKEYRRIIVSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 VTMFVVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIIYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 TLQLLEVWAVSELLLLPPILGIWGEMGI DEATESCTII KKEGBSIKKTI EVIGEI LECLV
                                                                                                                                                                           23 PSWLASALACVLI----FTIVVDILGNLLVILSVYRNKKLFNAGNIFVVSLAVADLVVAI 78
                                             94 FOLKETVVYILMDHWIFGALLORLMERVOOVVIVSVLSLVDIACHRHOOTIHPSSWKE- 152
                                                                                       79 YPYPLVLMSIENNGWNLGYLHOOVSGELMGLSVIGSIENIITGIAINBYCYICHSFKYDKL 138
                                                                                                                                34 PCWQSSTMTLTLVLCYCLVL1LGLLGNILLICIIMHQRDPPNVTSILIANLSVSDILVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000276; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berglund M.M., Starback P., Salaneck E., Gehlert D.R
                                                                                                                                                                                                                   Conservative 71; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                          18.7%; Score 339; DB 13; 26.3%; Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Commun 241:740-755(1997).
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RESULT 14
Q9NK26
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                                                                    RESULT 15
09NR49
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ΑIJ
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9NKZ5 PRELIMINARY, PRT: 392 AA.
O9NKZ6 C7000 (TremBLrel 15, Created)
O1-OCT-2000 (TremBLrel 15, Last sequence update)
O1-OCT-2000 (TremBLrel 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopteryyota, Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
Q9NR49;
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Submitted (CCT-1999) to the EMPL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 SNFRKDVASVVL 342
                                                                                                                                                                                                                                         319 NPIIYAASNRNYRVAYYKIFALL 341
                                                                                                                                                                                                                                                                                                                  291 NAIIYGLLNQNFRKEYRRIIVSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 IIVSYSGIYIIV------FHQKKKIRNHD--NFQIAAAKGSSSSGGGSYMTTTCTFKA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 TLQLLEVWAYSFLLLLPPILGIWGEMGLDEATFSCTILKKEGRSIKKTLFVIGFLLPCLV 213
                                                                                                                                                                                                                                                                                                                                                                                              264 REDNRLTVMMVTIFLCFLVCFLPL-MLANVVDDERNTSYP----WLHIIASVMAWASSVI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 -----VTMFVVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCL 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEVVEVLEAICWAPLNEIGLAVASDPASMVPRIPEWLEVASYYMAYENSCLNAIIYGLLN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCYVLLIMLTLAAVLENLRA - GTLQYDFRIYSCTEAQSVSSAYTIAVVVEHFLVEXII 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIAINRYCYI-CHSLKYDKLYSSKNS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASALACVLIFTIVVDILGNLLVILSVYRNKKLR-NAGNIFVVSLAVADLVVAIYPYPLVL 85
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                                  PRELIMINARY;
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Best Local 9
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"Cloning and characterization of the human HLWAR77, a G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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01-027-2000 (TremBirel 15, Last sequence update)
01-027-2000 (TremBirel 15, Last annotation update)
G-PROTEIN COUPLED PECEPTOP HIMAP77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coupled receptor.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF257210; AAF87078.1: -.
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                                                                                                                                                                                                                                                                                             154 LTLAAVLEN-----LRAGTLQYDPRIYSCTF---AQSVSSAYTIAVVVFHEL 197
                                                                                                                                                                       280 AFLSLIVIMYGRIGISLEKAAVEHTGPKNÇEQWHVVSEKKÇKI.... IKMILIVALL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 LIFTIVVDILGNLLVILSVYENKKLENAGNIFVVSLAVADLVVAIYPYPLVLMSIFNNGW 93
                                                                                                                                                                                                                                                                                                                                                                                      94 NLGYLHCQVSGFLMGLSVTGSTFNJTGTAINEYCYICHSLKYDKLYSSKNSLCYVLLIWL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                 54 LIFFLC -- MMGNTVVCFTVMRNKHMHTVTNLFILNLAISDLLVGIFCMPITLLDNIIAGW 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     local Similarity
                                        PKEYPPII-VSLCTAPVFFVDSSNDVADPVKWKPSPLMTNNNVVKVDS 349
                                                                                   FILSWLPL--WTLMMLSDYADLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENF
                                                                                                                            FAICWAFLNFIGLAVASDPASMVFR----IFEWLFVASYYMAYFNSCLNAIIYGLLNQNF 402
                                                                                                                                                                                                                VPMIIVIFCYLRIWILVL-------QVPQFVKPDRKPKIKPQDFRNEVTMEVVFVL 246
                                                                                                                                                                                                                                                         LAITIMSPSAVMLHVQEEKYYEVELNSQNKTSPVYWCFEDWPNQEMFKIYTTVLFANIYL
                                                                                                                                                                                                                                                                                                                                             FFGNTMCKISGLVQGISVAASVETLVAIAVDRFQCVVYPFK-PKL-TIKTAFVIIMIIWV
RRGFQEAFQLQLCQKPAKFME----AYALKAKSHVLINTSNQLVQES 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48686 MW;
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Search completed: February 18, 2001, 16:46:33 Job time: 8251 sec

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9b_9ss27.CNS04SOS
9b_9ss27.CNS04CH1
9b_9ss28.FET045DT0
9b_9ss28.CNS04T0
9b_9ss27.CNS04T0
9b_9ss27.CNS04T0W
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ab_qss27:CNS04VLK
qb_qss25:CNS01T3N
qb_ess75:BE798784
qb_ess75:BE798784
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qb_est25:AI820631
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qb_qss26:CNS03AWY
qb_est69 RE266564
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qb_est40:AW139137
qb_qss27.CNS03DQN
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qb_estbb:BE151339
qb_est23:A1693287
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qb_gss27.CNS040EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qb_est23.AI692402
ab_gss27:CNS04R4T
ab_est49:AW827034
gb_gss27:CNS03P70
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ab_est29.AU051007
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-Q-/QGR21/USFTC_Sp021X7SG0125945.7r.mat_0.6022001_133023_20600/app_qppry.fasta_1.413
-Q-/QGR21/USFTC_Sp021X7SG0125945.7r.mat_0.6021001
-GAPEXT -OFMT-fastap -SUFFIX-ret -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH-0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -FGAPOP=6.000
-FGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELD=6.000
-EGAPEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500 -DELD=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRE_SCOPE=pct -THE_MAX=100 -THE_MIN=0
-ALIGN=15 -MODE-LOCAL -COTFMT=pfs -NORM-EX-MAXISHO0 -THE_MIN=0
-ALIGN=15 -MODE-LOCAL -COTFMT=pfs -NORM-EX-MINEDHO
-MAXLEN=20000000000 -GSER=US09226046_@CGN1__12428 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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AL166028 Tetraodon nigroviridi
BE798784 601585581F1 NIFLMGC_7
AL5692402 wd6906.xi NCI CGAP_LU
AL210810 Tetraodon nigroviridis
AL25771 Tetraodon nigroviridis
BE266564 601193555F1 NIFLMGC_7
AL280651 Tetraodon nigroviridis
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| AL302248 Tetraodon nigrovirid
| AL291713 Tetraodon nigroviridi
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
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AL-105461 | G1-8197925
Css. gamemo survey sequence
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                                                                  Submitted (12-APP-2000) to the EMBL/GenBank/DDRJ databases. This sequence is a simple read and was demerated as part of a larscale closered sequencing project of the Tetraodon nigroviridis demons. For more information, Figase take a lock at
                                                                                                                                                                                     Direct Submission
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii: Ctenosquamata; Acanthomorpha; Euacanthomorpha;
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                                                ht*p://www.armoscope.cns_fr/Tetraodon
                                                                                                                                                                                                                  Genoscope.
                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holacantheptwrydii Acanthepterydii Percomorpha:
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                                                                                                                                                                                                                                                                                             Tetraodon pigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                             koest-Crolings, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "apublished
                                                                                                                                                                                                                                         (bases 1 to 842)
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                                                                                                                                                                                                                                                                                                                                                                                , Wincker, P., Brottier, P., Quetier, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                       Rouneau, L
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                                                    ELL CITTATAACITTCHTT#CARTEETAACITAAATETAAGACAGAGAGAGAGAGAGAGAGC
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22 ProLysteuLyser-GinAspPheAryAsnPheVallhimetFheValVa 243
                                                                                                                                                           561 AAATAACGTGIAGTCAGTAAIAIGCACACACCIAACACTGACCICIIGIC 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 uLeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuArqAlaG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 LeuLysTyrAspLysLeuTyrSerSerLysAsnSerLeuCysTyrValLe 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       §61 AAACAITIGGCCITICAGAAGIGAGCCCTIGTTTTCTTTAAATCTAAGAA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         561 COCCGCATCAGACCGAGTGACTTCAGAPATTTCCTAACCATGTTTGTGGT 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROPST-Crollius.H., Jaillon.O., Dasilva,C., Bouneau,L., Fish Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission

Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetracdon nigroviridis

genome. For more information, please take a look at

http://www.genoscoge.cns.fr/Tetracdon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 MetPhevalValPheValLeuPhcAlaIleCysTrpAlaProLeuAsnPh 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 rArgArgIleIleValSerLeuCysThrAlaArg 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 eIleGlyLeuAlaValAlaSerAspProAlaSerMetValProArqIleP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 CTACCTGCGCATCTGGATCCTGGTCATCCAGGTGAGGAGGCGGGTCAAGC 106
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V_type: phagemid
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Umrania, Y., Williams, G. and Brenner, S.
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Quality: 355.00
Ratio: 4.277
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                                                                                                                                                                                         Site lited (II-AFF-131) to the EMSL/JenBank/2FR3 databases. This sequence is a simule read and was generated at part of a large scale clone-end sequencing project of the Tetraodon nigroviridis denumber. For more information, please take a book at http://www.sequencings.fi/Tetraodon
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Human dene number estimate provided by denome wide analysis using Tetraodon cluroviridis PNA sequence
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Roest-Croilius,H., Jailion,O., Dasilva,C., Fizames,C.
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129000 of library o from Torrandon nigroviridis, genomic survey
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Percent Similarity, 71.642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               678 CATCGCCGCTCATGACCAACAACAACCAGGGTGAAAGTGGATTCGGTC 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         977 AAACITIGICACNCAIGIINGIGNIGIICGIGCICIINGCCGINIGCIGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 roSerProLeuMetThrAsnAsnAsnVal.ValLysValAspSerVal 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   927 GUGGEGNINAATTTNATORGEFFIRMNEIJARA GALCARACAAAAGGTGN 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 ATTATTANGGGGGGGGTTCTNNFGAFTSFGGGGGAGAGNCTCAAGAGCNANC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 lPhePheValAspSerSerAsnAspValAlaAspArqValLysTrpLysP 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheArgLysGluTyrArgArgTleTleValSerLeuCysThrAlaArgVa 318
                                                                                                                              Tetraodon nigroviridis
Envaryota; Metazoa, Chordata, Oranida, Vortobrata, Potoloostomi;
Envaryota; Metazoa, Chordata, Oranida, Vortobrata, Neotoloostei;
Acthiopterygii; Neopherygii, Televotei; Euteleostei; Neotoloostei;
Eutypterygii; Ctenosquamata, Acanthomorpha; Euacanthomorpha;
Edizanthoperygii; Acanthopterygii, Peremorpha;
Tetraodontiformes, Tetraodontuidai, Tetraodon, Tetraodon,
1 consolidae, Tetraodontuidai, Tetraodontiformes, Co., Fisher Co.,
Foest-Orollius, E., Jaillou, O., Dasilva, C., Fizames, C., Fisher C.,
Foencal, E., Filiault, A., Guetler, F., Saulio, K., Rernot, A. and
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Charaterization and repeat analysis of the compact genome of freshwater pufforfish Tetracies sizewinidis
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/clone="051019"
/clone_lib="A"
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|61 others
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PEFEPENCE
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Ratio: 1 31
Percent Similarity: 57.547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944 CTATCCACTACCCTTTCGTGTCATCCTTTACATGGTTTTAGGGGTCATTG 895
                                                                                                                                                                                                                                                                                                 694 AGTICIGATGIGATGITGIGCACAGCATCCATAATIAATCIGICITIAAI 645
                                                                                                                                                                                                                                                                                                                                               105 PheLeuMetGlyLeuSerVallleGlyScrIlePheAsnIleThrGlyIl 121
                                                                                                                                                                                                                                                                                                                                                                                                744 CGATAGAAACCTGCTGGTATTTTGGAGACATCTTTTGCAAAGTCCATTTG 645
                                                                                                                                                                                             644 ATCAATTGATCGATACAATGCGGTGATCCATCCTCTAGTGTATAGAAGAA 595
                                                                                            594 AAATGACTGGTCATGTTGTTTTGCTGATGATTTTTGTCAGCTGGAGTGIT 545
                                                                                                                                          138 euTyrSerSerLysAsnSerLeuCysTyrValLeuLeuIleTrp.
                                                                                                                                                                                                                                              121 eAlaIleAsnArqTyrCysTyrIleCysHisSerTenLysTyrAspLysL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 lAlaAspLeuValValAlaIleTyrProTyrProLeuValLeuMetSerI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 AsnLysLysLeuArgAsnAlaGlyAsnIlePheValValSerLeuAlaVa 71
544 TCAGGTGTTGTAGGTTTTGGAATGATTTTTTTAAGGCTGAACATTTGGGG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 leValValAspIleLeuGlyAsnLeuLeuValIleLeuSerValTyrArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 LeuAluSerAlaLeuAlaCys ValLeuTlePheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                              lePheAsnAsnGlyTrpAsnLeuGlyTyTLouHisCysGlnValSerGly 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STOTSACTTTOTOCTSGGGTTGTTGGTCATGTTACCCAATATGATTCAGA 745
                                           ....LeuLeuThrLecAlaAlaValLeuProAsnLeuArgAlaGlyTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases i to 1016)
Evest Crollius, E., Jaillon, O., Pasilva, C., Bouncan L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-ARR-2000) to the EMBI,/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.ons.ir/Tetraodon.
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2 (bases )
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/db_xref="taxon.99883"
/clone="129003"
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seq_name: gb_gss27:CNS04I2W
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ORGANISM
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                                                   AUTHORS
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                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 CAGCCAGAGATTCAAGTAAAAAAAAAAAAAAAAGCCACTAAAAACTCTTGTT 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 .....ATTCCAGGAATAATCATGATCAGTTTATACGTGAAGATTTTCTT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 PheLeuValProMetIleIleValllePheCysTyrLeuAigIleTrpIl 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 heAlacinSerValSerSerAlaTyrThrIleAlaValValValPhcHis 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 rLeuGla . . . TyrAspFroArgIleTyr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 rjLysFroLysLouLysProGlnAspPheArgAsnPheValThiMetPhe 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 eLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 TUTUTGTTACATCATTGATCCTTTTTTCAGCTACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 GTGATCATGGGAGCATTICTTTTATGTTSGACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 rpLeuPheValAlaSerTyrTyrMetAlaTyrPheAsnSerCysLeuAsn 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 CCICTOATHIATGCATTITTTACACCTGGTTTCGAAAGGGGTTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 AlaileileTyrGlyLeuLeuAsnGlnAsnFheArgLysGluTyrArgAr 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 CATTGTTTGANACATTCCTATGGCTAGGTTATATGAATTCTACACTAAAC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 .....IICCTGTTTGCTTCAGGAAAGGTCTTTAAAGAGGATATGTCAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 AC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValValFheValLeuFheAlaIleCysTrpAlaProLeuAsnPheIleGl 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon migrovinidis general survey sections T7 and of alone 111NO5 of library G from Tetraodon nigrovinidis, genomic survey
                                                                                                                                                                                      1 (bases 1 to 882)
Roest Croilius, H., Jaillon, C., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                       Eukaryota: Metaroa; Chordata; Craniata; Vertebrata: Fiteleostemi; Actinopterygii; Neopterygii; Teleostei; Euteleostei: Neoteleostei: Burypterygii; Ctenosquamata; Acanthomorpha: Euacanthomorpha: Holacanthopterygii, Acanthopterygii; Percomorpha: Tetraodontiomes; Tetraodontoidei; Tetraodontidac; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS; genome survey sequence.
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouncau,L., Fi
Bernot, A., Fizames,C., Wincker,P., Brottier,P., Quetier,F
                                                                                                                                Charaterization and repeat analysis of the compact genome of the \ensuremath{\operatorname{resnwater}} pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis.
Saurin, W. and Weissenbach, J
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                                                                       ., Fisher,C.,
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Ratio: 1.860
Percent Similarity: 58.140
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                                                          40% GGTCCTG1GGA1C1GGCTGCAGGCCCTGGCCAGC1GCTGGCCGCCGGCT1C 357
                                                                                                                                                                     4.5 GACTOTOTOCACTACAACTONOGCTGCACTGTGGGGTAGCTGTGCGGGT 409
                                                                                                                                                                                                                                                                                                                                   114 erilePheAsnileThrGlyIleAlaIleAsnArqTyrCysTyrIleCys 130
                                                                                                                                                                                                                                                                                                                                                                                             556 GOOCTOTOTTTGTACGGGTTACAGCTCCTCTGTGTGTACTCCACCGCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5 TOCACTGTATGTGTGGGCTGTTTAACATTTAATAATACCTANACACAGAC 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 rProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTyrL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 PheValValSerLeuAlaValAlaAspLeuValValAlaIleIyrProTy &1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 alileLeuSerValTyrArqAsnLysLysLeuArqAsnAlaGlyAsnIle 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (2 CysValLeuIlePheThrileVal.ValAspIleLeuGlyAspLeuLeuV 48
                                                                                                                                                                                                                    His Section by CytAsptysterdy: SectSectlysAsptertendysTy [47]
                                                                                                                                                                                                                                                                           TOTOTTOACOTTOACTATOCCCCT18ACCGGTACCAITCCAICAIG 457
rgAla...GlyThrLeuGlnTyrAspProArgIleTyrSerCysThrPhe 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOTANICCAGCCGILGEIAIGCAICGIGGGGIFICGFGIGGGGGGTGTAACA 889
                                                                                                        rValleuLeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/Tetraodon.
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1 MetGlnGlyAsnGlySer...
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Bernot,A., Fizames,C., Wincker,P., Brofffler,P., Queffor,F.,
Saurin,W. and Weissenbach,J.
Human dene number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APP-2000) to the EMBL/GenBank/DPBJ databases. This sequence is a single read and was generated as part of a latical clone-end sequencing project of the Tetrapodon nigroviridis genume. For note information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukarysta, Métarea, Cherdata; Craniata; Vertebrata; Estelecetei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctonosquamata; Ananthomorpha; Euaranthomorpha; Holacanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon. [ [ hages ] to [ 186 ]
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Belloom, Pilloult,A., Quetier,F., Sauris,W., Person,A. and
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/db_xref="taxon:99883"
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Persent Identity, 24,437
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281 TyrTyrMetAlaTyrPheAsuSerCysLouAso 291 :::::: 1048 TCIIGGATAAIGATGATTAATTCTTGTGTGAAC 1080	264 SpProAlaSerMetValProArgileProGluTrpLeuPheValAlaSer 2	• 247 eAlaIleCysTrpAlaProLeuAsnPheIleGlyLeuAlaValAlaSerA 2 : ::: :::::::::::::::::::::::::::::::	231 ProGlnAspPheArgAsnPheValThrMetPheValValPheValLeuPh 2	219GlnArqValLysProAspArqLysFroLysLeuLys 2:	204 ePheCysTyrLeuArgileTrpI]eLeuValLeuGlnValArq 27 	188 ThrileAlaValValPheHisPheLeuValProMetTleTleValII 20	ThrphoAlaGInSerValSerSerAlaTyr 18	159	ox on	129 leCysHisSerLeuLysTyrAspLysLouTyrSerSerLysAsnSerLeu 14	112 edlySerTlePheAsnIleThr@lyTl=AlazLeAsnArgTyrCysTyrI 12:	96 GlyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerValI1 11:	79 yrProTyrProLeuValLeuMetSerIleFheAsnAsnGlyTrpAsnLeu 95	62 yAsnilePheValValSerLeuAlaValAlaAspLeuValValAlaIleT 79	AC 38	IleLeuGlyAsn 4	12 rGlnProValLeuArgGlyAspGlyAlaArgProSerTrpLeuAlaSerA 29	199 ATGGATAGCAACGGGSACCCTTGGCTGTGGTTGGCTGGCCAACCTTAACTCCTC 248
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                                                                                                   149 TGCTTTCTATCATCTATTITAAGNAGCTCCACCTCCAACCAACTACCTG 198
139 INGSTOICIOINGCIGTUTCIGACTTTOTCCIGACGTTCTTTOTCATGTT 248
                                              66 ValValSerLeuAlaValAlaAspLcuValValAlaIleTyrProTyrPr 82
                                                                                                                                               49 leLeuSerValTyrArgAsnLysLysLeuArgAsnAlaGlyAsnIlePhe 65
                                                                                                                                                                                                   99 GTTCTAGGGGNCATGGTTGTTGTGACTGTGTGGGAAACCTTTTGGTCAC 148
                                                                                                                                                                                                                                                     33 ValLeuIlePheThrIleValValAspIleLeuClyAsnLouLeuVal I 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS04\overline{V}LK=1071\ bp DNA GSS 24-MAY-2000 Tetraodon nigroviridis genome survey sequence T3 end of clone 035005 of library A from Tetraodon nigroviridis, genomic survey
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GSS: genome survey sequence.
Tetraodon nigroviridis.
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Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,F., Brottier.P., Quetter,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pirect Submission submitted (12 APR-2000) to the EMHL/GenBank/DDBJ databases Submitted (12 APR-2000) to the EMHL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetrapace "igravitidis genome. For more information, please take a look at genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome. For more Intermediate http://www.genoscope.cns.fr/Tetraodon.Location/Qualifiers
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/dh_xref="taxon:99883"
/clone="035005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="A"
/note="Genoscope sequence ID : CUAAU35AH03Al-end : T3"
/note="Genoscope sequence ID : CUAAU35AH03Al-end : T3"
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Percent Identity: 26.214
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RIH alPhePheValAspSerSerAsn 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAGGAAGATGTATTTTATTTGAGAGTGGTATGTGAAGTAGAGTGTGGT 598
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                                                                 12-MAY-2000 Totraodon citroviridis decome survey sequence PUC-Cri end of ollower of library G from Tetraodon citroviridis, genomic surve sequence.
AL166028
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   3941084-15
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                                                                                                                                                                              872 PATROTOROGENIETE TELEVISIETE ANGESTANDEN STANDAROGENE STANDAROGEN STANDARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972 OCTAGGGAAATTGTGGTGATGTTATTGTGGGTGGAAGCGAAAGGGTTC
    822 GATGGG1
                                                                                                                                                                                                                                                                                                                                                                 922 CACTOSSTGACSTOSSTSCTSATCATAAACCTESCCGTCAGGGGAACGTGGT 873
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                                                                           92 lymmpAsnLeuSlymymLeuHisCysGlnValSer.......
                                                                                                                                                                                                                                                                        75 lValAlaIleTyrProTyrProLeuValLeuMetSerIlePheAsnAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 ArgAsnAlaClyAsnIlePheValValSerLeuAlaValAlaAspLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 eLeuGlyAsnLeuLeuValIleLeuSerVal.TyrArgAsnLysLysLeu 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 LeuAlaSerAlaLeuAlaCysValLeuIlePheThrIleValValAspIl 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-AFF-2006) to the EMRL/Deckark/HCE2 databases. This sequence is a single read and was acceptated as part of a large scale clone-end sequencing project of the Tetraodon midroviridis genome. For more information, please take a look at http://www.genoscope.com.fr/Terraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis
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Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1033) Frest-Crollius, H , J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holacanthopterygii; Acanthopterygii, Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodo:
1 (bases 1 to 1033)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene number estimate provided by genome wide analysis using Terrandon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
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/db_xref="taxon:99883"
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Fercent Identity: 23.952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 CISCACACIDESICCASESCASCAGAGATETGAACGCIGCITCICCITCC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 ATGTGAACATCALGAAGGIGGCACGAAGGCACGCCAGGAGGATCCACTCA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 yrteuArqTleTrpIleLeuValLeuGlnValAraGlnArqValLysPro 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 CICICCITCITGGCTCAGACCAGCTCGCAGGCACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 CCCGCAGCACCAAAACWFATNATGGAGTGG TTCGCCTCTTCCTGG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspArgLysProLys.LeuLysProGlnAspPheArgAsnPhe
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia; Eutheria: Frimatos: Catarrhini: Hominidae: Homo I (bases 1 to 861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE798784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE798784 861 bp mRNA EST 20-8EP-2000 601585581F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939741 5',
                                                                                                                                                                                                                                                                                                                                                                                                         RE798784 1 GI-10219982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluTrpfouPhoValAlaSorTyr 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProAlaSorMetValFroArgIlo 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .PheAlaTleCysTrpAl 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProLeuAsnPheIleG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyPheLeuMetG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACAACTC 83
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COMMENT
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US-09-226-046-12 x BE798784
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BE798784 from: 1 to. 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 CTAC.....AACTACTAIGCCACACIGCTCACCCIGCTCATCGCTGTCA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AACTEGAGCCGGCCCITCAACGGGTCAGACGGGAAGGCGGACAGACCCCA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                             227 TOGTCITUGGCAAUGIGUTGGTGTGCATGGUTGIGTUDCGDEADAAAARR 275
427 GTCATGATGTGCACGGCGACGATCCTGAACTTGTGTGATTAGTATTAG 476
                                                  108 GlyLeuSerVallleGlySerIlePheAsnIleThrGlyIleAlaIleAs 124
                                                                                                          377 GIGAGIGGAAAITCAGCAGGAITCACTGIGACAICIICGICACICTGIGAC 426
                                                                                                                                                                                                                        327 ΕΣΤΟΘΙΟΘΟΌΑΟΝΟΤΟΘΤΟΑΨΘΟΟΘΊΨΟΘΘΙΨΌΦΟΤΑΟΟΨΘΘΑΘΩΠΟΘΤΑΘ 376
                                                                                                                                                                                                                                                                                                                                277 CIGCAGACCACCAACTACCTGATCGTCAACCTGGCAGTGGCCGACCT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AsnAlaSerGinProValLeuArgGlyAspGlyAla.....ArgFroSe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 spileLeuGiyAsnieuLeuValIleLeuSerValTyrAigAsniysiys 57
                                                                                                                                                             91 smdlyTrpAsmLeuGlyTyrLcuHisCysClmValSerGlyPheLeuMet 107
                                                                                                                                                                                                                                                                       74 uvalvalnlaileTyrProTyrProLeuValLeuMetSerIlcPhcAsnA 91
                                                                                                                                                                                                                                                                                                                                                                                     58 LeuArgAsnAiaGlyAsnIleFheValValSerLcuAlaValAlaAspLe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 rTrpLeuAlaSerAlaLeuAlaCysValLeuIlcFhcThrIleValValA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.national Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: DCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 7
High quality sequence stop: 696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: LLCM789 row: a column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note**Organ: ling, Vector: pole?, Site_1: Nhc:, Site_2: corn: cDNA made by oligo-df priming, Directionally cloned into Ecorixonol sites using the following 5 cadedotor: GCACGAGG(C). Size-selected ~500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of G-raid M. Kutin (Giversity of California, Berkeley) using EAR-CCNA synthesis kit (Stratagene) and Superscript II RT (Dife Technologies)." a State California and Superscript II RT (Dife Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216.00
1.701
61.951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="small cell carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ceil_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 baps: 6
Percent Identity: 31.220
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 ACCATCTCC1GCCCACTCCTCTTCGGACTCATAACGCAGACCAGAACG... 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 ortysAsnSorLeuCysTyrValLeu...LeuIleTrpLeuLeuThrLeu 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 nArdTyrCysTyrIleCysHisserLeuLysTyrAspLysLeuTyrSerS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 qlleTyrSerCysThrPheAlaGlnSerValSerSerAlaTyrThrile, 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "12 CTACATCAAGATC 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaAlaValLeuPruAscLeuArgAlaGlyThrLeuGlnTyrAspFreAr 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTACACAGCTGTGGCCATGCCCATGCTGTACAATACGCGCTACAGCT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sTyrLeuArgIle 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaValValValPhoHisPheLeuValProMetIleIleValIlePheCy 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAACCGCGCGCGTCACCGTCATCATGTGCATGGTGTGGGGTGCTGTGTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOCALCUICICCITCIAC.....GIGCCCITCAIIGICACCCTGCTGGT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tound through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image html
Insert Length: 976 Std Frror: 0.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wd69b06 x1 NCI_CGAP_Lu24 Homo sapiens cDNA close IMAGE.2336819 37 similar to qb:M240b5 L(2) LOPAMINE PECEPTOR (HUMAN): mPNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fmail: Wobert_Strausbergamib gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmort-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Otrausberg, Ph.D. Tel: (301) 496-1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa: Chordata: Craniata; Vertebrata: Eutéleostomi:
Mammalla: Eutheria: Primates: Catarrhini: Hominidae: Homo
l (bases l to 753)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note-1988 http://www.orbi.nim.nih.gov/nciegap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Hento Soares, Ph.D. CDNA Library Arrayed by: Great Lengen, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xebul ones
/note-forgan lung: Vector pTTTD-Pac (Pharmacia) with modified polylinker: Plasmid finA from the normalized library NCI_CGAF_Lu5 was prepared, and as circles were made in wire Fell-wint MAP purification, this tAA was used as tracer in a subtractive hybridization reaction. The driver was PcR-amplified coMAS from a pool of 5,000 clones made from the same library (cionells
                                                                                                                                                                                                                                     /*ione="iMAGE:2436814"
/clone_lib="NCI_CGAP_Lu24"
/clone_lib="nci_cGAP_Lu24"
/iosur_"ype=" orelinid"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                         /ordanism="Homo sapiens"
/db_xref="taxon.9606"
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                                             ACCESSION
                                                                                                                                           DEFINITION
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PEATURES

COMMENT

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REFERENCE

SOURCE KEYWORDS ACCESSION

ORGANISM

DEFINITION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 uValValAlaIleTyrProTyrProLeuValLeuMetSerIlePheAsnA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 rTrpLeuAlaSerAlaLeuAlaCysValLeuIlePheThrIleValValA 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 OCCIDENACIOCETSATACOGSTCCTCTACATGCTCATCTTC. ....AT 145
                                                                                                                                                                                                                                                                                                                                                                                            146 ССІВВВЕТТЕТЕСЕВЕДАЛЕВЕЕТВЯТСАТЕТТЛАССВТЕТВВАЙАТССА 195
105 heLeuMetGlyLeuSerValIleGlySerIlePheAsnIleThrGlyIle 121
                                                        292 GCTGGGCTACCACTGGCCCTTCGGCGTCGCCCTGTGCAAGATCAGCAGCY 342
                                                                                                                                                                245 UNCCICACCITEGICGIO...ACCITACCCCTGTGGGGCGGTGTACACGCC 292
                                                                                                                                                                                                                                                                              196 AAFGGCMACGCGGGGCTGCMGACGTCTACATTGGAAACTTGGCTTTCGCT
                                                                                                                                                                                                                     72 AspLeuValValAlaileTyrProTyrProLeu ValLeuMetSerTl 88
                                                                                                                                                                                                                                                                                                                                   56 ysLysLeuArgAsnAlaGlyAsnIlePheValValSerLeuAlaValAla 72
                                                                                                                                                                                                                                                                                                                                                                                                                                              39 lValAspIleLeuGlyAsnLeuLeuValIleLeuSerValTyrArqAsnL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 ProSerTrpLeuAlaSerAlaLeuAlaCysValLeuIlePheThrIleVa 39
                                                                                                       88 ePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisCysGlnValSerGlyP 105
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Eukaryota; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi,
Eukaryota; Metazoa: Chordata: Craniata: Vertebrata: Euteleostei;
Actinopterygii: Neopterygii: Teleostei; Euteleostei;
Eurypterygii: Ctenosquamata: Acanthomorpha; Euacanthomorpia,
Holacanthopterygii: Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae: Tetraodon.
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Ratio:
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Tetraodon nigroviridis.
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POPST-Grollius H. Jaillon G. Dasilva G., Bouneau G., Fisher G.,
Bernot A., Fizames, C., Wincker, P., Brottrer, P., Quetier, F.,
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VERSION
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                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 hrLeuAlaAlaValLeuProAsnLeuArgAlaGlyThrLeuGlnTyrAsp 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 GCGCTCGCGCGCACCATGCTAGCGTCCCTGGGGCGCCATCTGTCTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 AGCTTOSATOGOYACCTOSCCATOSTGATTOCCTTTCCASCAGOCCCCT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 AAACCAGAAACACGAGCYGCTCTGGATCGCCGGGCTCAGTMTGTACTCCI 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 CAMAACAGCAACCGGACCACCIGOGGCATGGGACITCAGCCTGGTGACGGC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 FrcArgIlcTyrSerCysThrPhcAlaGlnSerValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 C36GCCTGCYGCCGGTGCCCACGCYGCTCTTCCGCACCACCTTGAACGAC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 uTyrSerSerLysAsnSerLeuCysTyrValLeuLeuIleTrpLeuLeuT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AlaIleAsnArgTyrCysTyrTleCysHisSerLeuLysTyrAspLysLe 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            819 GTTCTGAAGAGCATGGACGCCCTGTCCTACCTGAACCTGGCC 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 hrMetFheValValFheValLeuPheAlaIleCysTrpAlaPro .... 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 sproAspArgLysProLysLeuLysProGloAspPheArgAsnPhcValT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 TTCTACTGCWTCATCGGCTGCACCGTCACGCGCCATTTCAACAACCTG.. 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 CysTyrLeuArgIleTrpIleLeuValLeuGlnValArgGlnArgValL_{I}^{\prime} 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 leAlaValValPheHisPheLeuValProMetIleIleVal[lePhe 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 CCACGCTGGTG.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                             Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Poineau,L., Billault.A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Verlebrata, Euteleostoii, Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis
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                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact genome \mathbb{R}^{d+1}
                                                                                                                                                                                                                                                             Weissenbach,J
                                                                                                                                                                                                                                                                                                                                                                    Tetraodontiformes; Tetraodontoidei; Tetraodontidae;
                                                                                                                                                                                                freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                               (bases 1 to 982)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . ......GGTTTCCTCCTGCCTTTMCTGGCCATGAMCATC 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGTGTTCGCCATC16CIGGACICCCTTTCAC 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      982 bp
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                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon
                                                                                                                             Fisher.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 206.00
Ratio: 1.411
Percent Similarity: 55.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seq 1/2 to reverse of CNSCRAWY from 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09 226-046-12 x CNSOAAWY/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  819 GCCTCHHIGGCAACAEGHGCEATTTOCATAGACOGHTACCTGGCIA 770
                                                                                                                                                                         581 ATCTGTTCATFACAGII....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      769 CTCTCACCCACTGCICIATICCAAIAAGGTGACTGTGAAAAAGAGGGAAAA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            969 AAGSGCGTGCTGCTGTGGGTGTGGGATGTGGTGGTGGTGGTGGGGGGTGGT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOUTHOR
                                                             54: CITGATGIAGAGAGAGIGTTTGCAGCTGCTGTTGCTCAAATGCGAGTCAT 491
                                                                                                                  200 PhocysTyrLouArgIleTrp...IloLeuValLeuGlnValArg..... 218
                                                                                                                                                                                                                                       IPH hrileAlaValValPheHisPheLeuValProMetileIleValIle 204
                                                                                                                                                                                                                                                                                                                                                         176 rcys
                                                                                                                                                                                                                                                                                                                                                                                                                 RESENTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 LeuProAsnLeuArgAlaClyThrLeuGlnTyrAspProArgIleTyrSe 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      719 TTGCAATCTGTGTGTTTGGGCCIGHCIGIIITGIATAAGGGCIGTAII 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 ysTyrValLeulleTrpLeuLeuThrLeu......AlaAlaVal 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.7 oGysHisSerLeatysTyrAspLysLeuTyrSerSerLysAsnSerLeuC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GlySerIlePheAsnIleThrGlyIleAlaIleAsnArqTyrCysTyrIl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       869 GGAGTGTGATGTGTGCTGTGAGTGGTTATGTGTGGTAGTGTGTAGTTTGT 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            919 OGTGAIGCCGAICGAGGGGGTAGGGTAGGIGGAAAAAATGGTGGTGGTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 lyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyLeuSerValIle 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AsnilePheValValSerLeuAlaValAlaAspLeuValValAlaIleTy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 rProTyrProLeuValLeuMetSerIlePheAsnAsnGlyTrpAsnLeuG 96
                                                                                                                                                                                                                                                                                                  Submitted (12-APP-2000) to the EMHL/GonRank/DONG databases. This sequence is a single read and was generated as part of a large scale clone end sequencing project of the Tetrack-oneign whild is genome. For more information, please take a look at http://www.cengescope.com/fr/Tetrack-one http://www.cengescope.com/fr/Tetrack-one
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                                                                                                                                                                                                                                                                                                                                                                                                                    ....ATOGGCCACCICAAACAICCAGACAGGIACAGIIC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="010316"
/clone_lib="C"
/not=="Genoscope sequence ID : COBG016DE08SE1-end
PUC-Ori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:9988%"
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1. .982
.GlmArgValLysProAspArgLysPrzLysLeuLysP 271
                                                                                                                                                                                                                                                                                                                                                      ....ThrPheAlaGlnSerValSerSerAlaTyrT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 c
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                                                                                                                                                                                ...GITTTCCCCIGIGCCATCATGGTT 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION FULLY (555F) NIH_MAX_7 Home sapiens conA clone IMAGE.3537589 5%
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1171F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTRACTOR TO THE CONTRACTOR TANDAMENT ASSOCIATION OF THE CONTRACTOR OF THE CONTRACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 roGlnAspPheArgAsnPheValThrMetPheValValPheValLeuPhe 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 TOSTETGOAGAAOSOGSOGTGGGTGGGAGGAGGAGGAGGAGGGTGAAAA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 TrTTrMctAlaTyrPhcAsnScrCysLeuAsnAlaIlcIlcTyrClyLou
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NIH-MGC http://www.ncbi-nim-nih-nov/MGC/.
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Plate: LLCM221 row: m column:
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/cell_line="MGC3"
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OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

February 18, 2001, 20:17:47

Scarch time 3705 49 Seconds (without alignments) 1197.437 Million cell updates/sec

Run on:

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Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database

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Searched:

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SUMMARIES

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Conservative
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/dene="hMella"
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Homo sapiens clone RP11-45C13, WORKING ERAFT SEQUENCE,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone Rp11-45C13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-NoV-1999) Whitchead instruction, MI) confor for Gouome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Sequence version replaced gitq103498. On Aug 26, 2000 this sequence version replaced gitq103498. All repeats were identified using RepeatMasker: All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Sequencing vector M13; M77815; 100% of reads Sequencing vector M13; M77815; 100% of reclimistry Dye terminator Big Dye; 100% of reclimistry Program: Phrap; version 0.960731
Assembly program: Phrap; version 0.960731
Consensus quality: 137351 bases at least 040 consensus quality: 143518 bases at least 030 Consensus quality: 145518 bases at least 020 consensus quality: 145518 bases at least 030 consensus quality: 145518 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
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137507 137606: gap of 137607 149317: conti
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92640 15366, contin of 12727 bp in length
105557 10545b; gap of 100 bp
105467 12cuser contin of 14594 bp in length
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7260 8782: contin of 1523 bp in length
8783 8882: map of 100 bp
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17945: gap of 100 bb
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196. .11727
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25230: contig of 2610 bp in length
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50637 TICAGGAAGGAATACAGGAGAATTATAGTCTCGCTCTCTCTACAGCCAGGGTGTTCTITGTG

718 ttcaggaaggaatacaggagaattatagtctcgctcgtgacagccagggtgttctttgtg 777

50577 GACAGCTCTAACGACGTGGCCGATAGGGTTAAATGGAAACGGTCTCCACTCATGACCAAC 50518

778 gacagototaacqacqtqqooqataqqqttaaatqqaaaccqtotocactqatqaccaac 837

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HSU14108

1085 bp

50517 AATAATGTAGTAAAGGTGGACTCCGTTTAA 50488

838 aataatgtagtaaaggtggantccgtttaa 867

SOURCE ORGANISM

REFERENCE

TITLE AUTHORS

REFERENCE

95033233 Reppert

(bases 1 to 1085)

AUTHORS TITLE JOURNAL MEDLINE

Direct Submission

JOURNAL.

Submitted (29-AUG-1994) Steven M. Reppert, Chronobiology, Children's Service, Massachusetts General Hospital, 32 Fruit St. Boston, MA 32114, USA

FEATURES

80 JUN 8

/sex="male and female" /dev_stage="adult" 33...1085

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Location/Qualifiers

DEFINITION ACCESSION HSU14108

Human Mel-la melatonin receptor mRNA, complete cds

01-NOV-1996

VERSION

U14108.1 GI.602129

KEYWORDS

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50877 AAACCTGACCGCAAACCCAAACTGAAACCACAGGACTTCAGGAATTTTGTCACCATGTTI 50818

478 aaacctgaccgcaaacccaaactgaaaccaacacttcaggaattttgtcaccatgttt 537

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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini: Hominidae; Homo. 1 (bases 1 to 1085)
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SGFLMGLSVIGSIFNITGIAINRYCYICHSLKYDKLYSKNSLCVYLLIWLLTITAAVL
SGFLMGLSVIGSIFNITGIAINRYCYTHSLKYVYHFLYWMITVIFCYLRIWILVIQVR
PNLRAGFIFYLDYCDFRAGVTMFVVFVLFAICWAPLNFIGLAVASDPASMVPRLFEWL
CXYKYDBFFYLDYCDFRAFVTMFVVFVLFAICWAPLNFIGLAVASDPASMVPRLFEWL
FVASYYMAYFNSCLNAIIYGLLNQNFFKEYRRIIVSLCIAKVFFYLJSSNLVAJENYKWE
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ReppertLS.M. and Ebisawa,T.
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Pirron B. Linton L. Nusbaum, C., Lander, E., Allen, N., Anderson, M. Baldwin, J. Harna, N., Beckerly, K., Boyuslavkiy, L., Bukhqalter, R., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymorc, A., Brown, A., Colley, M., Collins, S., Collymorc, A., Cooke, P., Dearelland, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Firreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
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______ project Information
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34293: qap of 100 bp
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64621: contig of 812 bp
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Fred. No. 1.3e-127;
0; Mismatches 151; Indels 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloning and characterization of a mammalian melaconin receptor that mediates reproductive and circadian responses Neuron 13 (5), 1177-1185 (1994)
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1 (bases 1 to 1149)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pars tuberalis (pituitary)"
/dev_stage="adult"
49. .1149
                                                                                                  VVFCYLRIWALVLOVPWKVKPONKPKLKDODFRNEVIMEVVFVLEAICWAPLNEIGLV
VASDPASMAPRIPEWLEVASYYMAYENSCLNAIIYGLLNQNERQEYRKIIVSLCTTKM
EFVDSSMHVADRIKPKPSPLIANHNLIKVDSV"
                                                                                                                                                                TLASILIFTIVVDIVGNLLVVLSVYRNKKLRNAGNVFVVŠLAVADLLVAVYPYPLALA
SIVNNOWSLSSLHCQLSGFLMGLSVIGSVFSITGIAINRYCCICHSLRYGKLYSGTNS
LCYVFLIWTLTUVAIVPNLCVGTLQYDFRIYSCTFTQSVSSAYTIAVVVFHFIVPNLV
                                                                                                                                                                                                                                                /product="Mel-la melatonin receptor"
/protein_id="AAB17721.1"
/db_xref="GI:502132"
                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male and female"
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/db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 /note="high-affinity receptor"
                                                                                                                                                                                                                            /translation="MAGRLWGSPGGTPKGNGSSALLNVSQAAPGAGDGVPPRPSWLAA
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  Unknown
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DNA encoding high-affinity melatonin receptors
Fatent: US 5856124-A 3 05-JAN-1999;
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Children's Service Massachusetts
Boston, MA 02114, USA
On Nov 1, 1996 this sequence vers
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Weaver, D. R., Liu,C. and Reppert, S.M.
Nature's knockout: The Mollb melatonin receptor is not necessary
for reproductive an circulian responses in Siberian harsters
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"Indiag and characterization of a mammalian momentates reproductive and circudian responses Neuron 13 (5), 1177-1185 (1944)
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QVRBEVKASYYMAYENSLLNALTYGLLNWIPPGFYKFILVSIFTAKMCFYUSSNUPADKI 
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/product="melatorin receptor Mel-la"
/protein_id="AAB17722.1"
/db_xref="c1-1654110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male and female"
/hissue_typo:"hypothalamus and pituitary pars tuberalis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="A146"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          geotetyaceesyceageatgetgectaggateccagagtggetgtttqtqqqqattae 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTCAGACCCTGCCACCATGGCCCCCAGAGTGCCCAGAGTGGCTGTTCGTGGCTAGTTAC 852
                                                                                                                                                                                                                                                                                                                                                                         Ovis aries Mel la melatonin receptor mRNA, complete cds. \Delta F0.45219
Barrbtt,P., Conway.S. and Morgan P J
Direct Submission
Submitted (28-JAN-1998) Mol. Endocrinol. Unit, Rowett, Greenburn
                                                                                                    1 (bases 1 to 1219)

Barrett,P. Gonway,S., Jockers,R., Strosberg,A.D.,

Guardiola-Lemaitre,B., Delagrange,P. and Morgan,P.J.

Cloning and functional analysis of a polymorphic variant of the ovine Mel la melatonin receptor

Riochlm Biophys Acta 1356 (3), 209-307 (1997)
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THE THE TRANSPORTED THE THE THE TRANSPORTED TO THE THE TRANSPORTED TO 
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/db_xref="G1:2865611"
/db_xref="G1:2865611"
/db_xref="G1:2865611"
/db_xref="G1:2865611"

TLASILIFTIVDIVGNILVVLSVYRNKKLRNAGNVEVVSLAVADLLVAVYPYPLALA
SILNINGSSEGTLWGLSVIGSVESITGIAINRYCCIOHSLRYGKLYSGTNS
SIVNNGWSLSSLHCOLSGELMGLSVIGSVESITGIAINRYCCIOHSLRYGKLYSGTNS
CCYVELIWILIVAIVPNLCVGTLOXDPRIVSCIETOGVSSAYTIAVVVEHEITVPNLV
CCYVELIWILIVAIVPNLCVGTLOXDPRIVSCIETOGVSAVTIAVVVEHEITVPNLV
VVFCYLRIWALVLQVRWKVKPDNKPKLKPQDFRNEVTMFVVFVLFAICWAPLNFIGLV
VASUPDSMAPRIPEWLFYASYYMAYFNGCLNAITYGLLNQNFPGFYPKITVSLCTTKM
VASUPDSMAPRIPEWLFYASYYMAYFNGCLNAITYGLLNQNFPGFYPKITVSLCTTKM
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Submitted (25-MAR-1996) Steven M. Reppert, Pediatrics,
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Peppert, S. M. and Ebisawa, T.
ENA encoding high-affinity melatonin receptors
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Saisonnieres, CNRS-UMR 7518, Universite Louis Pasteur, 12 Rue de
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GLSVIGSIENITGIAINRYCYICHSLKYDRLYSNKNSLCYVELIWVLTLVAIMPNLQT
GTLQYDPRIYSCTETRSVSSVYTIAVVVEHEIVPMIIVIECVIEIWILVLQVPREVKP
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/protein_id="AAC67241.1"
/db_xref="GI:3779236"
/translation="LMASQQAPGGGEGGRPRPSWLASTLAFILIFTIVVDILGNLLVI
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Submissed (59-SEP-1996) Animal Sci
Kildee Hall, Ames, IA 50011-3150,
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U73327 1 31.2135528
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Rothschild, M.F
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Womack,J.E., Parendse,W., Crawford,A.M., Notter,D.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BTU73327
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Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovoidea:
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202 c 184 q 215 t
                                                                /product-"melatonin receptor IA"
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//deno-"MINRIA"
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//deno-"melatonin receptor la from sheep, encoded by
denBank Accession Number #14108, and from human, encoded
by denBank Accession Number #14104"
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Barendee,W., Crawford,A.M.,
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                                                                                               655 tactacatggsyta***-caaragetgesteaatgesattatatatgggetastggaascaa 714
                                                                                                                                421 GTGAAAGGTGAGAAGAAAGGGAAAGTGAAGGGGAGTTCAGGAATTTTGTGAGGATT
                                                                                                                                                                                                                                                                                                                                                    241 CCCAACCTGTGTGGGGGACCCCCCAGTACGACCCGACGATCTATTCCTGTACCTTCACG
                                           661 AATTTCAGGCAGGAATACAGAAAAAITATAGTCTCAITGTGTACCACCAAGATGTTCTTT
                                                                                      601 TACTATATGGGATATTTCAAMARITGCCTCAATGCGATCATATATGGGACTACTGAACCAA 660
                                                                                                                                                                                                                                                                                                                                                                 181 ACCAUGAATTOCCTOTOTOCTACGTOTTOCTOALALOGATGATGATGATGCTCGTGGCGATCGTG
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Search completed: February 19, 2001, 00:51:31 Job time: 16424 sec

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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                  Result
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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The queue has been cloned by polymerase chain reaction amplification of human genomic DNA, using primers derived from the Xenopus laevis melatonin receptor sequence (709947), and use of the product as a 20 probe on a human genome library in phage EMBL-3 under high stringency. The 5'-portion of the yene has been obtained by reprobing the DNA library at low stringency and the complete sequence is given in 70950. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor agonists or receptor antagenists. Agonists may be used in therapy of circulation for specific actions the such as jet-lag or day night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to receptor dene may also be expressed in a transgenic animal for use one a model system to screen agonists and antagonists.
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compounds, by measuring changes in metabolic activity. The recombinant human metatonic receptor protein is useful as it has the same activity natural human melatonic receptor protein. The new screening method is bottor than prior attractivements assay techniques at quantitatively determining melatonic, which uses antibodies produced by linking
                                                                                                                                                                         melatonin receptor protein, which comprises an animal cell containing an expression plasmid for the gene encoding a human melatonin receptor protein. The cells are useful for screening for human melatonin receptor fracteins and its assauls of assauls to a become and synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melatonin to a carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 qtcaqtqqgttcctqatqggcctqaqcqtcatcggctccatattcaacatcaccggcatc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 gecateaacegetaetgetaeatetgecaeagteteaagtaegaeaaactgtaeageage 423
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                                                                                    1024 aataatgtagtaaaggtqqactccgtttaa 1053
                                                                                                                                                                                                       718 ttcaqqaaqqaatacaqqaqaattataqtctcqctcqtqacaqccaggqtqttctttqtq 777
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                                                                                                                                                 838 aataatgtagtaaaggtggactccgtttaa 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gragittitateetttttaeeatttaetaggeteetetgaaetteattageetaggeegig 597
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Pred. No. 26-225;
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creceptor, which is a membrane protein, coupled to quantine nucleotide countries (G-proteins). The genc has been cloned by binding protein (G-proteins). The genc has been cloned by could protein reaction amplification of human genomic DNA, using CC polymerase chain reaction amplification of human genomic DNA, using CC primers derived from the Xenopus laevis melatonin receptor sequence cc primers derived from the Xenopus laevis melatonin receptor sequence cc isolation of the full-length clone. Primers 10955-56 amplify a cc isolation of the gene, and have been used with probe 70992 to cc interact with melatonin, or specific antibodies, may be used as complete the tissue distribution of this gene for comparison which cc interact with melatonin, or specific antibodies, may be used as complete disorders, to control ovulation, or in alteration of cycle disorders, to control ovulation, or in alteration of the sequence of the seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The interaction of the interaction of the interaction of the interaction of the receptor and as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty; antibody; transgenic animal; drug screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High-affinity melatonin-la receptor gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melatonin-la receptor; human, G-protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-1996 (first entry)
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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17-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MASS-) MASSACHUSETTS GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 5; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-058368/06.
                                                                                                                                                                                                                                                                                                                                                                                                     The sequence encodes full-length human high-affinity melatonin-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                               Sequence 1085 bf, 120 A, 120 C, 270 G, 257 T; 0 other)
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       95.0%:
       Score 823.6; DB 17; Length 1085; Pred. No. 2c-225;
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                                                                            Molatonin receptor protein: buman: chinese bamster ovary cell: CHO cell: job lam: sleeplessuess, scasonal melancholia; Alzhelmer's disease, domontia: cerebral thrombosis: high blood_pressure; cancer; melancholia;
                                      ovulation regulator; neurosis; mental confusion; glaucoma; therapy; ds
                                                                                                                                                                                                                                                                        Melatonin receptor protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                         23 JUN-1997 (first entry)
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DB 18; Length 1050;

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                                                                                                                                              melatonin receptor agonist can be used as an agent for preventing or treating jet lag sierpiessness, seasonal melancholia. Altheimer's disease, dementia caused by censor thrombosis, various diseases accompanying againg, high blood pressure, cancer, and glauroma. The melatonin receptor can also be used as an ovulation regulator. The melatonin receptor antavenist can be used as an agent tor preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the coding sequence for the human melatonin receptor protein. This sequence is used in an expression vector designated parks observed the expression vector is used to produce the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant human malatonin receptor protein and (ant)agonists used for treating jet lag, Alzheimer's disease, melanchoila, neurosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     chinese hamster avary (CHO) sells of the invention. The CHO oclis express the human melatonin receptor protein, and can be used to identify compounds (such as agonists and antagonists) having affinity to the receptor. The choosing also be used to produce the receptor. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-252999/23.
P-PSPB: W15786.
Sequence 1050 BP; 216 A; 310 C; 257 G; 257 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2: Page 15: 21pp; Japanese.
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                                                                                                       treating melancholia, neurosis, or mental confusion.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; cyclediation; reproductive cycle; animal breeding; puberty;
                                                                                                                                                                                                                                                                                                                                                                                                antibody; transgenic animal; drug screening; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T09948 standard; DNA; 1149
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                                                                                                                                                07-OCT-1994;
                                                                                                                                                               06-JUN-1995;
17-JUN-1994;
                                                                                                                                                                                                        07-JUN-1995;
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DNA encoding high affinity melatumin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian
                                                                                                                  (MASS:) MASSACHUSETTS GEN HOSPITAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberalis mRNA, using primers derived from the Xenopus laevis melatonin receptor sequence (T09947), and use of the product as a probe on a sheep pars tuberalis cDNA library and a sheep genomic therein the contract of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins). The gene has been cloned by reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhythm disorders or reproductive cycles
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880 geoteggaeceegeeageatggeaeceaggateeeegagtegetgtttgtggftagttae 939
                                     598 geotetgaececgecageatggtgectaggateceagagtgaetgtttgtggecagttae 657
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Nucleic acid comprising melatonin la receptor promoter and reporter done—used to transform cells for screening for agents that alter transcription from promoter, e.g. for correcting circadian rhythm
                                           WPI; 1998-120701;11
P PSDB; W23958.
                                                                                                                                                                                                                                polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse melatonin la receptor gene.
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                                                                                                                                                                                                                                                                                                                                                                                       promoter
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Matches 702: Conserv
disorders or controlling reproduction in animals
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Pred. No. 1.4e-158;
o. Mismatches 165; Indels 3
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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty; antibody; transgenic animal; drug screening; ds.
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                                                                                                                                                                                                                                                                                                                                                                         DNA encoding high affinity melatonin receptor one – used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
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                                                                                      proteins (Oproteins) The dene has been closed by the course R2-2 transcription-polymerase chain reaction amplification of mouse R2-2 man. The corresponding genomic DNA consists of 2 exciss divided by mRNA. The corresponding genomic DNA consists of 2 exciss 444 bp a large (over 8 kb) intron. The 3 unitianslated region is 444 bp a large (over 8 kb) intron. The 3 unitianslated region A major long, and includes the polyadenylation signal AUUAAA. A major long, and includes the polyadenylation south 100 bp upstream of the transcription start site is located about 100 bp upstream of the initiation codon. Receptor fragments which interact with initiation codon. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists melatonin, or specific antibodies, may be used in therapy of or receptor antagonists. Agonists may be used in the provided the polyadenylation as set-lag or day-night cycle.
                                                                                                                                                                                                                                                                                                                                       Claim 9; Fig 3; 115pp; English.
                                                                                                                                                                                                                                                which is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins). The gene has been cloned by reverse
                                                                                                                                                                                                                                                                                         The sequence encodes a mouse high-affinity melatonin-la receptor
circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The
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RESULT
T79066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1002 BF: 262 A. 277 C: 241 G. 282 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 gggaatatatttgtggtgagtttagotgtggcagacotogtggtggctgtttae0ottat 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 gtcagtgggttcctgatgggcctgagcgtcatcggctccatattcaacatcaccggcatc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 cocttggtgctgacatctatccttaacaacggatggaatctgggatatctacactgtcaa 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 aagaaetegetetgetaegtgtteetgatatggatgetgaeaeteategeeateatgeee 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 gocatcaaccyctactyttacatctyccacaytctcaaytycyacaaactytacaycayc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 gtcagogcatttctaatgggcttgagtgtcatcggctcgatattgaacatcacggggatc 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 aaceteegtegtgggaeteteeagtaegageegaggatetaetegtgeacettegeecag 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 atagtoatottotqttacotqaqaatatqqatootqqttotocaqqtoaqacaqaqqqtq 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 teceficagetececetacaccategeogtegtegttttteceaettectectectececateate 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggaaacatetttgtggtgagettageggtggcagaeetggtggtggeeatttateegtae 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613 attgtcatcttctgctacttaaggatatgggtcctggtccttcaggtcagacggagggtg 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 totgtoagotoagogtacacgatagoagtggtggtttttocatttcatcgtgcotatgatt 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 amacoogacamcamgoocmamactgamgooccmggmacttcmggmactttgtcmccatgttc 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 aaacotgacogcaaacccaaactgaaaccacacgacttcaggaattttgtcaccatgttt 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 giggittitgicottittgccattigctgggctcctctgaacticatiggcclggccgig 597
                                                                   1033 aataactteeteeeggtggaetetgtttaa 1062
                                                                                                                                                                                                                                                                                                                                                                                        598 goototgaccocgccagcatggtgcctaggatcccagagtggctgtttgtggccagttac 657
                                                                                                                                                                                                                                                                                                                   658 tacatggcgtatttcaacagctgcctcaatgccattatatcgggctactggaaccaaaat 717
                                                                                                                                                                                                                                                                                                                                                           793 gootcagacootgooacoatggtooccaggatoocagagtqgotgttogtggctagttac 852
                                                                                                                                                                                                               913 trcagaaaggaatacaaaaagattartgtctcgttgtgcacagccaagatgttctttgtg 972
                                                                                                    838 aataatgtagtaaaggtggactccgtttaa 867
                                                                                                                                                                         778 gacagototaacqacqtqqccqatagqqttaaatggaaaccgtotocactqatqaccaac 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccgttggtgctgatgtcgatatttaacaacgggtggaacctgggctatctgcactgccaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aagaaotocototgotaogtgotootoatatggotootgao---ggoggoogtootgoo 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aacctgcaaaccggaacactccagtacgatccccggatctactcctgtaccttcacccag 552
                                                                                                                                                                                                                                                                                                                                                                                                                                gtagttittgtacttittgccarttgttgggccccactcaacctcataggtcttattgtg 792
                   ω
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                                                                                                                                                                                                                                                                                    tacctggcgtacttcaacagctgcctcaacgcaattatatacqgactactgaatcagaat 912
                                                                                                                                        gagagttoamatgamgamgomgatmagattaddlytdagsoctolocaetamlarnosat 1032
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Pred. No.
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Best Local Similarity 66.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences 17906 cob represent sovel allelt gases of the Xesspus lavys melatonin receptor MEL-1A. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. This sequence is a short form of the novel receptor MEL-1Ab also known as Mol 1-c(beta). As compared to the short form (179066), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mPNA. The MEL-1Ab sequences also differ from known MEL-1A receptor sequences by a mino acids. The nucleotide sequence was isolated from cDNA derived from knoppus skin RNA and amplified using the primers 179067-76. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allele: Xenopus laevis: melatonin: receptor: untranslated region: PCR: mPNA: halt-life: skin: amplification: primer: polymerase chain reaction: transmembrane domain: cellular signalling; inhibition: adenylyl cyclase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1147 BP; 313 A; 245 C; 240 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike MEL-lAa (T79053) cannot inhibit adenylyl cyclase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-1Ab has been shown to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding functional melatonin receptor of Xenopus tor screening for potential (ant)agonists useful for e.g. treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ADIR ) ADIR & CIE.
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121 atmosfqqqffortgatqqqrriqaqqqfratqqqrtqqatattqaaqatqanqqqqtq 180
                                                                                                                                                                                                            259 coqqitaattotoataqotattittooaqaatqqqtqqacqottqqaaatatocattqtoaq 318
                                                                                                             61 coqtiqqtqetqatqtoqatattdacaacqqqtqqaacetqqgetatctqcactqccaa 120
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                                                                                                                                                                               Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The MEL-lab sequences also differ from known MEL-la receptor sequences by 6 amino acids. The nucleotide sequence was isolated from coNA derived from Xenopus skin RNA nucleotide sequence isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence and amplified using the primers T79067-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling MEL-lab has been shown to modulate intracellular CCMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike MEL-laa (T79063) cannot inhibit adenylyl phosphodiesterase, but unlike MEL-laa (T79063) cannot inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
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Pred. No. 2.2e-101;
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                                                                                                                                                                                                                                                                                                                                                                         Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR; mpNA; half-life: skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus melatonin receptor MEL-1Aa short form coding sequence.
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cardiovascular disease and cancer
            New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for c.g. treating
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                                                                                                    Marullo S,
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859 thraiggrotaitttaaragttytotoaatyotyttatatatyytytyotaaatoaaaao
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nilarity 66.2%;
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Pred. No. 4.9e-100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA; half-life; skin; amplification; primer, polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenyly; cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss
                                                                                                                                                                                                        Claim 1; Page 25:26, 62pp, French.
                                                                                                                                                                                                                                  cardiovascular disease and cancer
                                                                                                                                                                                                                                            New nucleic acid encoding functional meiatonin receptor of Xecopus for screening for potential (ant)agonists useful for e.g. treating
                                                                                                                                                                                                                                                                                P-PSDB; W25926
                                                                                                                                                                                                                                                                                             WPI; 1997-132625/12
                                                                                                                                                                                                                                                                                                                    Juckers R. Marullo
                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9704094-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allele, Xenopus laevis, melatonin; receptor, untranslated region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T79063 standard; cDNA to mRNA; 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1039 aacaatcaagcagatatgtac 1059
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                                                                                                                                                                                                                                                                                                                                                                    54 - mt. 1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus melatonin receptor MEL-1Aa long form coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= MEL lAa receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                    Strosberg AD
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sequences enough the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from CDNA derived from Xebergus skin sNA and amplified using the primary 17067.76 The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalizing. MEI-lAA has been shown to inhibit adentity operate, but both proteins can modulate intracellular cOMMP, rep inhibiting its accumulation induced by an inhibitor of the previously known proteins. This sequence is a long form of the novel receptor MEL-1Am also known as Mel 1-c(alpha). As compared to the short form (179004), the difference occurs in the 3 unitaristated region (both Sequences 17-weak-by represent movel alimin ander of the Abbuquas laevis melatonin receptor MELIA. The sequences enough proteins which are 65 amino acids shorter than those described in the prior art. Also the late of terminal amino acids encoded by these sequences are different from phosphodiesterase. Also the last

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Query Match

h 44.3%; Similarity 66.2%;

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RESULT 12
T09952
AC XX
             T09952 standard, cDNA: 1105 RD
T09952;
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δδ В

61 cogftggfgcfgafgtcgafafttaacaacggglegaaactgggglatstjesetsccaa 120

1039 aacaatcaagcagatatgtac 1059

838 aataatgtagtaaaggtygac 858

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sequence 1311 BP; 369 A; 259 C; 209 C; 414 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 atcaqtygottcctgatgggactcagcgttattggatcagtottcaacataacagccata 378
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                                                                                                                                                                                                                                                                        garagetetaacqaeqtqqeeqafaqqqttaaatqqaaaaccqtetecaetqatqaeccaac 837
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prod. No. 5.2e-100;
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                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day:night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty; antibody; transgenic animal; drug screening; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melatonin-1b receptor; human; G-protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which is a membrane protein, coupled to guanine nucleotide binding proteins (G-proteins), and has been cloned by PCR amplification of human genomic DNA, using primers based on the 3rd and 6th transmembrane domains of the xenopus sequence (T09947), then transmembrane domains of the interest of the xenopus sequence (T09947), then transmembrane domains of the interest of the interes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MASS-) MASSACHUSETTS GEN HOSPITAL.
                                                                                                                                                                                                                                                                                                       receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans be receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an intron of about 9 0 kb in the 1st cytoplasmic loop region. Intron PCR with primers T09953-54 and 43 human-rodent somatic Intron PCR with primers T09953-54 and 43 human-rodent somatic cell hybrids has been used to localize the human MURTHB gene to chromosome 11q21-22. Primers T09955-56 and probe T09961 have been used to analyse tissue distribution. Receptor fragments which used to analyse tissue distribution antibodies, may be used as interact with melatonin, or specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhythm disorders or reproductive cycles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R88414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence encodes human high-affinity melatonin-1b receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Fig 6; 115pp; English
                                                                                                                                                                                                                                                      Sequence 1105 BP; 188 A; 363 C; 303 G; 251 T; 0 other:
235 ggtaatttgttottggtgagtotggcattggctgacctggtggtggccttctacccctac 294
                                                                                                                                                Local
                              1 ggaaacatotttgtggtgagottagoggtggcotggtggtggtggcoatttatoogtac 50
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                                                                                                                    560;
                                                                                                                                             h 44.3%;
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                                                                                                                    Conservative
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                                                                                                                           0;
                                                                                                                                                   Score 383.8; DB 17; Length 1105; Fred. No. 6.3e-100
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ci;cadian rhythm disorder; jet-laq; day-night cycle disorder
condation; reproductive cycle; animal breeding; puberty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T09947 standard; cDNA; 1320 BP
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                                                                                                                                                                                                                                                    antibody; transgenic animal; drug screening; ds
                                                                                                                                                                                                                                                                                                                                                                                                           Molatonin receptor, o protein coupled receptor, melanophore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High-affinity melatonin receptor gene
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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor-agonists or receptor-antagonists. Agonists may be used in the tag of circudian rhythm disorders such as jet lag or day night cycle disorders, to control ovolation, or in alternation of reproductive cycles in seasonally broading animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human melatonin receptor sequences. Receptor fragments which interact with melatonin, or specific antibodies, may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consensus sequence for initiation of translation. The Xenopus sequence has been used for isolation of homologous sheep, make
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Xenopus dermal melanophores, and expressed in Escherichia col
Flanking ENA sequences of the 1st 2 Met ocdeds both display a Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encodes a high-affinity melatonic receptor from Xenopus laevis. The receptor is a membrane protein, coupled to quantine successful the first proteins (G proteins). The cDNA has been simpled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Parading high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animal for use as a model system to screen agonists and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                Corn barnacle; G-protein; binding receptor; secondary gene; ship;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn barnacle G-protein binding receptor secondary gene.
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corn barnacle G-protein binding receptor secondary gene - useful to develop protection against corn barnacle attachment, e.g. to bottoms of ships, wharf(s) and drainage
                                                                                                                                                                                    13-MAR-1996;
                                                                                                                                                                                                                                                  JP09248185-A
                                                                                                               (KAIY-) KAIYO BICTECHNOLOGY KENKYUSHO KK
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                                                                                                                                                                                                                                                                                  /product= "G-protein binding receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     industry. The corn barnacle G-protein binding receptor secondary gene, which is involved in the mechanisms of such attachment, can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a corn barnacle G-protein binding receptor secondary gene. Corn barnacles, which attach themselves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridisation. E. coli JMl09 carrying the plasmid PCC-PARZ, which contains the corn barnacle G-protein binding receptor secondary quality been deposited as FERM P-15509 with the National Institute of
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                                                                                                                                                                                                                                                                                                                                                  Human; alpha-1C adrenergic receptor; tissue specific receptor expression: reverse transcriptase-polymerse chain reaction; RT-PCR; heart mRNA; transmembrane region; primer; open reading frame; bowine; hippocampus; alpha-1C receptor, library; mammalian cell line; ligand; truncation; function; signal transduction signal; beniqn prostatic hypertrophy; finasteride; intraocular pressure; arrhythmia; CNS; prostatic cancer; male pattern baldness; seborrhoea; temale hissulism, prostatitis; acne; potassium channel opener; minoxidil; G-protein; ligand binding site; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q72224 standard; cDNA: 921 BP
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                                                                                                                                                                                                                                                                                                 Synthetic.
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(MERI ) MERCK & CO INC
                                                             15-MAR-1993;
                                                                                                                       10-MAR-1994;
                                                                                                                                                                                 29-SEP-1994.
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Pred. No. 9.9e-09;
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Best Local Similarity
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used to detect selective inhibitors of alpha IC, useful for
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Search completed February 18, 2001, 20:25:27 Job time: 12991 sec

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Cupyright (c) 1993 - 2000 Compuses Utd
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RESULT 1 US-08-466-103A-5 US-08-466-103A-5 Sequence 5. Application US/08466103A Barent No. 5856124 GENERAL INFORMATION: ARABATION: APPLICANT: Reppert, Takashi TITLE OF INVENTION: HIGH-AFFINITY MELATONIN TITLE OF INVENTION: RECEPTORS AND USES THEREOF NUMBER G: SEVICURCES: 29 COPPERSYONDENCE ADDRESS: APPLEASESEE: Fish, Fichardson P.C STREET: 225 FRANKlin Street CITY: Boston STATE: MA STATE: MA STATE: MA STATE: MA STATE: MA COUNTRY: US COMPUTER READABLE FOPM: COMPUTER READABLE FOPM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE OF MINDOWS Version 2.0 CURRENT APPLICATION NUMBER: US/08/466,103A APPLICATION NUMB	54 6.2 2140 2 US-08-244-354-1 33 54 6.2 2140 3 US-08-244-354-1 34 6.2 2140 3 US-08-244-354-1 35 54 6.2 2140 3 US-08-26-299-1 36 6.2 2140 4 PCT-US95-07180-1 37 51.8 6.0 1280 1 US-08-192-288-1 38 51.8 6.0 1280 1 US-08-192-288-1 39 50.8 5.9 7218 1 US-08-232-46-3-1 39 50.4 5.8 1167 1 US-08-232-46-1 39 50.4 5.8 1167 1 US-08-232-46-1 39 50.4 5.8 1167 1 US-08-496-095-1 39 50.4 5.8 1239 1 US-08-496-09-21-2 41 50 5.8 1239 1 US-08-233-09-22 42 50 5.8 1239 1 US-08-233-09-22 43 49.6 5.7 1872 1 US-08-233-09-22 44 49.6 5.7 1872 1 US-08-233-2848-39 45 49.6 5.7 1872 4 PCT-US93-11153-39 ALIGNMENTS
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                           Sequence II, Application 08/08466198A Patent No. 5856124
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GENERAL INFORMATION:
APPLICANT: Repper
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Local Similarity 100.0% Prod. No. 4.6e-223;

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TITLE OF INVENITON: HIGH-AFFINITY MELATONIN
TITLE OF INVENITOR: PECEPTOPS AND USFS THEFEOF
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MEDIUM TYPE: Diskett
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SOFTWARE: FastSEQ for Windows Version
CHPRENT APPLICATION DATA:
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                                                                                 241 aagaaotooototgotaoqtgotootoatatggotootgao---agoggoogtootgooo 297
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Patent No. 5856124
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APPLICANT: Reppert, Steven M.
APPLICANT: EDISAWA, TAKASHI
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
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         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319
FILING DATE: 07-007-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/261
APPLICATION UMBER: 08/261
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,815
REFERENCE/DÜCKEI NUMBEF: 0
TELECOMMUNICATION INFORMATION
TELEPHONE: 617/542-5970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence LOCATION: 49...1146 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 gtcagtgggttcctgatgggcctgagcgtcatcggctccatattcaacatcaccggcatc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 70.6%;
Local Similarity 82.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 aagaactccctctgctacgtgctcctcatatggctcctgacg---gcggccgtcctgccc 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 gocatcaaccgctactgttacatctgccacagtctcaagtgcgacuaactgtacagcagc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ccgttggtgctgatgtcgatatttaacaacgggtggaacctgggctatctgcactgccaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 aacctccqtcqtqqqactctccaqtacqaqccqaqqatctactcqtqcaccttcqcccaq 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  580 AACCTGTGTGTGGGGACCCTGCAGTACGACCCGAGGATCTATTCCTGTACCTTCACGCAG 639
                                                                                                                                                                                                                                                                                                                          478 aaacctgaccgcaaacccaaactgaaaccacacgacttcaggaattttgfcaccatgttt 537
                                                                                                                                                                                                                                                                                                                                                                 769 GTAGTOGTOTOTOTTACOTGACAATOTGGGCCTGGTTCTTCACGTCAGATGGAAGGTG 759
                                                                                                                                                                                                                                                                                                                                                                                                418 ataqtoatottotqttacorgaeaatatygateetggttotoogggtoaganagaqqqtq 477
                                                                                                                                                                                                                                                                                       760 AAACCGGACAACAAACCGAAACTGAAGCCGCAGGACTTCAGGAATTTTGTCACCATGTTT 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ggaaacatctttgtggtgagcttagcggttggcagacctggtggtggccatttatccgtac 60
718 ttcaggaaggaatacaggagaattatagtctcgctcgtgacagccagggqtgttctttqtq 777
                                                                                                                                  820 GTGGTTTTTGTCCTCTTTGCCATTTGCTGGGCTCCTCTGAACTTCATTGGTCTCGTTGTG 879
                                                         940 TATATGGCATATTTCAACAGCIGCCICAATGCGATCATATATGGACTACTGAACCAAAAT
                                                                                             658 tacatggcgtatttcaacagctgcctcaatgccattatatcgggctactggaaccaaaat 717
                                                                                                                                                                   598 geetetgaecoogcoageatggtgeetaggateccagagtggetgttttgtgggccagttac 657
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pred. No. 6.7e-155;
0; Mismatches 151; Indels 3;
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                                                                                                                                                                            Query Match 68.1%; Score 560; 148.3; Bost Local Similarity 80.7%; Pred. No. 9.4e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
    1522 COLLIGITATICACATCTATCCTTAACAACAAAAGAATCTGGGATATCTACACTGTCAA 1581
                                                                              REFERENCE/DECKFI NUMBER: DETELECOMMUNICATION INFORMATION: 517/542-507
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TITLE OF INVENTION: MELATIONI IA MECEFTUR GENE
TITLE OF INVENTION: PEGULATORY PEGIONS AND USES THEREOF
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                         PEATURE
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NAME: Fraser. Tanks &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1120 CATAACCTAATAAAGGTGGACTCCGTTTAA 1149
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SOFTWARE: FASTSF2 for Windows Vorsion 2 H
URRENT APPLICATION DATA:
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                                       61 continuityatyonatatttaacaacqqqtqqaacctqqqctatotqcactqccaa 120
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CLASSIFICATION:
                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding sequence LOCATION: 1270...2328
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                                                                                                                                                            Conservative
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                                                                                                                                                                                                 Fig. 3: Length 2772;
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US-08-466-103A-13 Patent No.

Sequence 1%, Application ${\rm PS}/{\rm PH455103A}$ Patent No. ${\rm S856124}$

GENERAL INFORMATION:

APPLICANT: Reppert, Steven M. APPLICANT: Ebisawa, Takashi

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

ZIP: COUNTRY · CITY: Boston

02110-2804 Ä S

COPPESSONNENCE ADOPESS:
ADDRESSEE: Fish & Richardson P.C STFEET. 225 Franklin Street

NUMBER OF SEQUENCES:

TITLE OF INVENTION: HIGH-AFFINITY MPLATONIN FECEPTORS AND USES THEREOF

Takashi HIGH-AFFINITY MELATONIN

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                                                                                                                                                                                                                              1942 AAACCCGACAACAAGCCAAACTGAACCCCAGGACTTTGAGGAACTTTGTGACCATCTTC
                 838 aataatgtagtaaaqqttqqactccqtttaa 867
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(1)
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                                             guongothtuangangiggongalagggithadatggababoniththobactbabtgabonabo 837
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                                                                                                                                                                    goototgamoogooagoatggtgootaggatoocagagtggotgtttgtagooagitac 657
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US-08-466-103A-13
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SEFERENCE/DOCKET NUMBER 0078

TELEFONE: 107542-5070

TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.1 Matches 697; Conservative
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FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 GGGAATATATTTGTGGTGAGTTTAGCTGTGGCAGACCTCGTGGTGGCTGTTTACCCTTAT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence LOCATION: 1...1059
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                       433 AAGAACTEGGTGTGCTACGTGTTTCCTGATATGGATGCTGACACTCATGGCCATCATGCCC 492
                                                                                                                                                                                                                                                                                                                                                                                                                    181 gecateaacegetactgttacatetgecaeagteteaagtgegaeaaactgtacageage 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 GTCAGCGCATTTCTAATGGGCTTGAGTGTCATCGGCTCGATATTGAACATCACGGGGGATC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 CCCTTGGTGCTGACATCTATCCTTAACAACGGATGGAATCTGGGATATCTACACTGTCAA 312
                                                                                                                                                                                                                              493 AACCTGCAAACCCCAACACTUCAGTACSATCCCCGGGATCTACTCCCGGTACCTTCACCCAG
                                                                                                                                                                                                                                                                        298
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                                                                        613 ATTGTCATCTTCTGCTACTTAAGGATATGGGTCCTGGTCCTTCAGGTCAGACGGAGGGTG 672
                                                                                                                                                                         358 tecqteageteegeetacaceategeegtqqtqqtttttccaettectegteeeatqate 417
673 AAACCCGACAACAAGCCCAAACTGAAGCCCCCAGGACTTCAGGAACTTTGTCACCATGTTC 732
                    478 aaacctgaccgcaaacccaaactgaaaccacacgacttcaggaattttgtcsccatgttt 537
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                                                                                                                                                                                                                                                                 aaccteeqteqtqqqqeteteceaqtacqaqeeqaqqatetacteqtqcacetteqeecaq 357
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                                                                                                                                                                                                                                                                                                                                                                                     GCTATGNACCGTTACTGCTACATTTGCCACAGCCTCAAGTACGACAAAATATACAGTAAC 432
                                                                                                           nucleic acid
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17-JUN-1994
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                                       MOLECULE TYPE:
                      FEATURE
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER
                                                                            STRANDEDNESS:
                                                                                              TYPE:
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                                                           TOPOLOGY:
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NAME: Fraser, Janis K.

PEGISTRATION NUMBER: 34,819
REFERENCE/EUCKET NUMBER 0079
REFERENCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                    INFORMATION FOR SEQ ID NO: 15.
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                     FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
AFFLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEO for Windows Version CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                       SEQUENCE CHARACTERISTICS:
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EDNESS: double
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Ebisawa, Takashi
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07-OCT-1994
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                                Sequence 1. Application US/OR4F6104A
Patent No. 5856124
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GENERAL INFORMATION:
APPLICANT: Repper
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                                                                                                                                                                                                                                                *18 ttraggaaggatgttegggagagatatagtctegetegtgaeageeagggtgttetttgtg 777
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OTHER INFORMATION
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Reppert, Steven M
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IIILE OF INVENTION: HIG
TITLE OF INVENTION: PEC
NUMBER OF SEQUENCES: 29
COFFESSONLENCE APPRESS:
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSPQ for Windows Version 2 0
OURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,103A
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PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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ATTOFNEY/AGENT INFORMATION.
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298 adootooytegtaggaattiteedaataegaategaagatetaetegtgeaenttiqoocodd 357
                                                                                                476 ARAARANTIRATATI HILLI HILL
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                                                                                                                                                                                                                                                                                                                  290 CCGGTCATTCTCATAGCTATTTTCCAGAATGCATGGACGCTTTGGAAATATCCATTGTCAG 349
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OTHER INFORMATION:
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REGISTRATION NUMBER:
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06-JUN-1995
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55 1%; Pred No 5 le-93;
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Sequence 17, Application US/08722001
Patent No. 5760054
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APPLICANT: Nerenberg, Jennie R
APPLICANT: Lee, Hee-Yoon
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
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ADDRESSEE: Merck & Co., Inc.
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COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatertIn Release #1 0 Version #1.25
SOFTWARE: PATERTIN DATA:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 14-APR-1995
                              ATTORNEY/AGENT INFORMATION:
                                                                                                          CLASSIFICATION: 514
                                                                                                                            FILING DATE:
                                                                                                                                          APPLICATION NUMBER: US/08/722,001
                                                                                                                                                                                                                                                                                               COUNTRY:
NAME: Appollina, Mai
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gacagototaacgacgtggccgatagggttaaatggaaaccgtotocactgatgaccaac 837
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                                                                                                                                                                                                                                                                                                                                                       126 Lincoln Avenue
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                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                         Floppy disk
                  Mary A.
                                                                            08/229,276
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US-08-722-001-17
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US-08-722-001-24
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TELEX: 138825
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Sequence 24, Application US/08722001 Patent No. 5760054 .
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TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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TOPOLOGY: bo
                                                                                                                                                                                       APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-Yoon
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                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                               TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS NUMBER OF SEQUENCES: 35
                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 OCCTTOTATGCCCTCTTCTCCTCTCTGGGGCTCCTTCTACATCCCTCTGGCGGTCATTCTA 668
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              STATE: New Jersey COUNTRY: United States of America
ZIP: 07065
                                                                                           ADDRESSEE:
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                                                                           126 Lincoln Avenue
                                                                                                  Merck & Co.,
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47.0%; Pred. No. 4.4e-07;
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engineen 1. Application de,/maian749 patent No. 6031090
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    Sequence 1 Application MS/09130749
    Patent No. 6031344

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                                        US-09-130-749-1
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THEOPMATION FOR SEQ ID NO: 1:
SEQUENCE CHAPACTERISTICS:
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                                                                                                                  432 ACCOSTACCTCCST98GRAPHACHTHUGGTIAAGGTCAAGCTGCTGTCTCCTCAGGCGG 391
                                                                                                                                                                                                                                                                                                                                                                ziz opportigiajojeamantionasportspanarojeamanosisisseentenarootae 271
                                                                                                                                                                                                                                                                                                                                                                                    68 tgotgatgtogatattthacaargggtggaarctgdgriatctgccaagtcadtd 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: HS/09/130,749
FILING DATE: 07-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOOKET NUMBER: GP-70513
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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COMPUTER READABLE FORM:
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ADDRESSEE: PATNEP & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSHOURBAGY, NABIL ELSHOURBAGY, NABIL OF LOVENTION: MOLECULAR CLONING OF A 7TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHABON, USMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Valley Forge STATE: PA
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REGISTRATION NUMBER: 23,031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 610-407-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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            RESULT 12
US-08-334-698-3
Sequence 3, Application US/08334698
Patent No. 5556753
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APPLICANT: SHABON, USMAN
AFFLICANT: ELSHOURBAGY, NABIL
TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
TITLE OF INVENTION: RECEPTOR (GPR31A)
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 143;
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REGISTRATION NUMBER: 23,031
REFERENCE/POCKET NUMBER: GP-7
TELECOMMUNICATION INFOEMATION:
TELEPHONE, 610-407-0700
TELEPAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versicn 2.0
CURRENT APPLICATION DATA:
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TELEFAX: 01.
TELEFAX: 01.
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COMPUTER: TRM Compatible
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                                                                                                                                                                                                                                                                                                                                                                             152 TOTACCTSCTCANCCTSSCHOTGSCTGANTTSCTGCTGCCTGCCTTTCCTGG 211
                                                                                                                                                                                                                  332 ACCRETACCTCCCTGTGGTGCACCCTCGGCTTAAGGTCAACCTGCTGTCTCCTCAGGCGG 391
                                                                                                                                                                                                                                                       188 acceptactettacatcteccacaetctcaaeteceaactetacaactetacaecaecaecaecaect 247
                                                                                                                                                                                                                                                                                                  PIZ GITTOFTGCTGGACCTCAGCGGAGCGTGGGATGGGCCTTCCTGGCCGCCGTGGCTTTGG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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FILING DATE: 07-AUG-1998
                                                                                                                                       392 COCTGGGGGTCTCGGGCCTGGTCTGGCTCCTGATGGCCCCTC 435
                                                                                                                                                             248 ccetetgetacgtgetecteatatggetectgacggeggeegte 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 58.4; DB 3; Length 96C; Local Similarity 53.4%; Fred. No. 1.1e-06; nes 143; Conservative 0; Mismatchec 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  68 tgctgatgtcgatatttaacaacgggtggaacctggggtatctgcactgccaagtcagtg 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 tetttataateatettaaegataaeaaaeetaataataaeeattateeataeeeattaa 67
                                                                                                                                                                                                                                                                                                                                    ggtteetgatgggeetgagegteateggetecatatteaacateaceggeategeeatea 187
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O Box 980
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TELECOMMUNICATION INFORMATION:
IELLIHONE: (212) 977-9550
TELERAX. (212) 423523 COOP UI
INFORMATION FOR SEQ ID NO: 3.
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TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic TITLE OF INVENTION: Receptors and Jses Thereof NUMBER OF SECTENCES 6

CORRESPONDENCE ADDRESS.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FROM PC COMPATING SYSTEM: PC-DOS/MS-
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AFFLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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LENGTH: 1738 base pairs
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ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/334,698
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                                                                                                                                                                                                                                                                       424 fremendegeocciasasgrectiogetiacidosiscophishocoarcitététéAcate 483
                                                                                                                                                                                                                                                                                                                                               NAME: White, John P. REGISTRATION NUMBER: 28 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                     604 AAGUCCATCITGGCGCTGCTCAGTGTGTGGGGTCTTGTCCACCGTCATCCCATCGGGCCT 663
                                                                                                                                                           184 atcaaccgctactgttacatctgccacagtctcaagtgcgacdadctgtacagcuscaag 243
                                                                                                                                                                                              484 TGGGCAGCCGTGGATGTCCTGTGCTGCACAGCGTCCATTCTGAGCCTGTGCGCCATCTCC
                                                                                                                                                                                                                                 124 agtgggttcctgatgggcctgagcgtcatcggctccatattcaacatcaccquidity 00 080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 124..16
CTHER INFORMATION:
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304 cgtcgtgggactclcoaglacyadocga...ggatctactcg+qcacct+cgcccadtcc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS.
                                                                                                                                                                                                                                                                                                        64 ttggtgotgatgtogatatttaacaacgggtggaacotgggctatotgcactgccaavtc 123
                                                                                                                                                                                                                                                                                                                                                                   4 aacatotttgtggtgagcttagcggtggcagacctggtggtcgccatttatccgtacccy 63
                                                                                      aactooctotgetacgtgetecteatatggetectgacggeggeegtectgeecaacete 303
                                                                                                                       10112
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47.6%; pred. No. 1.5e-06;
vative 0; Mismatches 223; Indels 3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFLECTION NUMBER: 41x7
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 477-4550
TELEFAX: (212) 425-23 CCCP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                               Ouery Match
Best Local similarity 47.6%;
Matches 20%; Conservative (
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ATTORNEY/AGENT IMPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
FITLE OF INVENTION: USE OF ALPHA-IC SPECIFIC COMPOUNDS TO TREAT BENICH
FILE OF INVENTION: PROSTATIC HYPERPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM
444 AACTACTTCATTGTCAACCTGGGCATGGGCGAGCTGCTGGAGGTTGAGGTTGAGGGTGCTGGGG 423
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LOCATION: 124..1683
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERALING SYSTEM: PC-DUS/MS-DUS SOFTWARE: Patentin Release #1.24
                                     64 tiggiqciqaiqicqaiaittaacaacqqqtqqaacctqqqctatctqcactqccaaqtc 123
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Fred. No. 1.5e-05;
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US-08-468-939-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 278-04'
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CVEFMAINS SYSTEM: PC-10-5/MS-100S
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTOPNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTPATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READARLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                 ANTI · SENSE.
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                                LOCATION: 124..1683
OTHER INFORMATION:
                                                                                                                             NAME/KEY
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1185 Avenue of the Americas
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                                                                 ATIORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 237-0400
TELEPAX: (212) 331-0526
INFORMATION FOR SFQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application 45/08406855A Patent No. 5851309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic TITLE OF INVENTION: Receptors and Uses Thereof NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Relicuration DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 TGGGCAGCCGTGGATGTCCTGTGCTGCACACCGTCCATTCTGAGCCTGTGCGCCCATCTCC 543
                    SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
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COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DUS/MS-DOS
SOFTWARE: Patentin Release #1.30
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Local Similarity 47.6%; Pred. No. 1.5e-06;
hes 205; Conservative 0; Mismatches 223; Indols 3; Gaps
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SUMMARIES

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ALIGNMENTS

VERSION KEYWORDS	ACCESSION	RESULT 1 CNS05KTS/c LOCUS DEFINITION	
AL341929.1 GI:8235687 GSS: genome survey sequence.	sequence. AL341929	CNSO5KTS 1101 bp DNA GSS 26-MAY-2000 Tetraodón nigroviridis genome survey sequence T3 end of clone 042G01 of library A from Tetraodón nigroviridis, genomic survey	

Qy 73 Db 74 Qy 79	0 7	Qy 616 Db 861	QY 556	Qy 496	Qy 437 pb 1041	Oy 377 Db 1101	Query Mat Best Loca Matches	BASE COUNT ORIGIN	FEATURES Sourc	TITLE JOURNAL COMMENT	JOURNAL REFERENCE	TITLE	JOURNAL REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS	SOURCE ORGANISM
6 agaattatagtotegetegtdacageggggtt. Engly Philippe 11111111111111111111111111111111111	gcattatatogggctectggaaccaaattcaqqaaqaadatta	atggtgcctaggatcccagagtggctgtttgtgggccagttartscatggcgtatttraac 6	qenatttgetgggeteetetgaaetteartggeetggeegtageetetgaeeegeeage 61 	aaactgaaaccacacgacttcaggaattttqtcaccatgtttgtggtttttqtcctttt 55	tgagaatatggatcctggttctccaggtcagacagagggtgaaacctgac-cgcaaaccc 49	tettetgttace 43	ch 25 1% Source 217.2 pR 193: Length 1101: 1 Similarity 67.1%: Pred No 5.8e-49; 331; Conservative 0; Mismatches 160; Indels 2; Gaps	/clone="042G01" /clone_11b="A" /note="Genoscope seq 297 a 240 c 211 q	9 H		Unpublished 3 (bases 1 to 1101) Genoscope.	Saurin, w. and weissemback, or the provided by genome wide analysis using Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	Fisher r,F.,	Weissenbach, J. Charaterization and repeat analysis of the compact genome of the Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	i (bases 1 to 1101) Roest-Crollius, H., Jailloc. F., Wasilva, C., Fizamos, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and	Tetraodon nigroviridis M Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Teleostei; Butolocstei; Neoteleostei; Actinopteryqii; Neopteryqii; Teleostei; Euacanthomorpha; Eurypteryqii; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Holacanthopteryqii; Acanthopteryqii; Percomorpha; Holacanthopteryqii; Tetraodontioldei; Tetraodontidae; Tetlaodon.

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502 aaaccacacgacttcaggaattttgtcaccatgtttgtggttttttgtcctttttgccatt 561
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Tetraodon nigroviridis genome survey sequence T7 end of clone
099D15 of library G from Tetraodon nigroviridis, genomic survey
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GSS; genome survey sequence.
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Bernot,A., Fizames.C., Wincker,P., Brottzet,F., yuctier,F.,
Saurin,W. and Weissenbach,J.
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/db_xref="taxon:99883"
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Submitted (11-001-1999) MRC Human Genome Mapping Project Resource
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Fukaryota: Metazoa: Chordata: Craniata: Vertebrata: Actinopterygii:
Neopterygii: Teleostei: Euteleostei: Acanthopterygii: Percomorpha:
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C: Mismatches 53;
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                                                                                                                                                                905 CTGGNNGTAG-AGATGAGAGAAAAGGTGNTGTCNTCCTNAFCCTTGAGTGGTTATTNGTG 848
                                                                           649 gccagttactacatggogtatttmaamagminimitmatgonattatatingiigintactgg 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-AFF-2009) to the EMRL/GenRunk/FirBJ databases. This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracelor digroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burdo gene number estimate provided by genera wide analysis using Tetraodon nigroviridis DNA sequence
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Rowst-Ciclius, H., Jaillon, C., Easilva, C., Rouncau, L., Fis

Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F.

Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-APR-2000) to the EMBL/GenBank/FDBT databases. This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weissenbach,
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Direct Submission
Submitted (11-OCT-1999) MKC Human Genome Mapping Project Resource
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biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
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Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
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                                                                                                                                                                                                                               CNSOSROS
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Class: BAC ends
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Plate: 670 row: O column: 5
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Mahairas, G.G. Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Kollor, A., Shakor, P., Furlong, T., Young, J., Zhac, S., Adams, M. B.
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BE654347 510 bp mPNA EST 06-SEP-2000 ULLM-AGG-AGG-E-11-9-HI FI NIH BMAP_MPG MUS musculus cDNA clone ULLM-AGG-AGGI il-0-UI 5', mENA sequence.
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Eurypterygii: Otenosquamata, Acanthomospha; Euroarchomorpha;
Holacanthopterygii: Acanthopterygii: Percomorpha;
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Furnan gone number estimate provided by genome wide analysis using Tetracoon nigroviridis DNA sequence
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Rouneau, I., Billault, A., Quetier, F., Saurin, W., Bernot, A.
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., Wincker,P., Brottler,P., Quetier,
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237 ANGGGGATGTT350GCTCCTCASTGTGTGGGTGTGTGTGGACGGTGATG 344
                                          244 aactocototgotacqtqctcctcatatqqctcctgacggcggccgtc 291
                                                                                                237 ATTGACCGCTACATTGGGGTGCGATACTCTCTGCAGTACCCCACGCTGGTCACCCGCAGG 296
                                                                                                                                             184 atcaaccgctactgttacatctgccacagtctcaagtgcgacaaactgtacagcagcaag 243
                                                                                                                                                                                                                                                                                                                                                                                                     - J
                                                                                                                                                                                                                                                                                                                                             64 ttggtgctgatgtcgatatttaacaacgggtggaacctgggctatctgcacctgccaagtc 123
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97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301 443 1706
Fax: 301 443 9890
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by Bonaldo, Lennon and Soares, Genome Research, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories."

a 267 c 129 g 128 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host-"DH10B (Life Technologies)"
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I, Site_2: Eco RI; The NIH_BMAP_MPG library is a non-normalized library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UI-M-A00-acf-f-11-0-UI"
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/dev_stage="27-32 days"
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RESULT 10

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1 (bases 1 to 740)
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Department of Zoology
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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87; Conservative 0, Mismatches 224: Indels
                                    AW966793 666 bp mRNA EST 01-JUN-2000 EST79867 MAGE resequences. MAGE Homo sapiens cDNA, mRNA sequence.
AW966793.1 GI:8156629
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/db_xref="taxon:7719"
/clone="rcitb15h19"
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                                              Mammalia: Eutheria: Rodentia, Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 669)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Londacre, S., Mahmoud, M., Meenen, E., Federsen, I., Peilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, P.
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The Institute for Genomic Research
9712 Medical Center Dr., Pockville, MD 20850, USA
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 301 838 0208
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Insert Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                   ATCAGCAGCYACGTGGTTCTGGTCAACATGTAGGCAGCGTTTTCTGGGTTGAGGTGGCTC 392
                                                                                                                                                                                                                                                                                                                                                                                     175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12 APR-2000) to the EMBL/GenBank/DDBJ databases. This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roest-Grollius.H. Jaillon O. Pasilva.G., Rouneau.L. Fish Bernot,A., Fizames,G., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Métazoa: Chordata: Craniata: Vertebrata: Euteleostomi Actinopterygii; Neopterygii; Teleostoi: Euteleostei. Neotcleoste Eurypterygii; Ctenosquamata: Acanthomorpha: Buacanthomorpha: Holacanthopterygii, Acanthopterygii; Percomorpha: Tetraodontiformes: Tetraodontoidel: Tetraodontidae: Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charaterization and repeat analysis of the compact genome of the
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Poest-Crollius, H., Jaillon, O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="160024"
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## 20.200;
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نائد
                                                                                                                                                                                                                                                                                                                                                                                Score 53.4; DB 191; Length
Fred. No. 0.00051;
5; Mismatches 186; Indels
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REFERENCE
AUTHORS
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KEYWORDS
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R15256
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                                                                                                                          BASE COUNT
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                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R15256 466 bp mPNA EST 13-APR-1995 yf89d03.rl Soares infant brain INIB Homo sapiens cDNA clone IMAGE:29866 5' similar to gb:M64749 G PROTEIN-COMPLEM PECEPTOR PDC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,E., Williamson,A., Wohldmann,P. and Wilson,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 303 Source: LMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1857 Std Error 0 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park, Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 466)
Hillier.L., Clark.N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                     double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III strates of the Lafmid BA vector Library went through one round of normalization, library constructed by Bento Soares and M.Fatima Bonaldo."

a 141 c 109 g 119 t 3 others
                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                                                                                                                                                                                                                                                                               I - oligo(dT) primer [5′
ΑΑCΤGGAAGAATTCGCGGCAGGAATTTTTTTTTTTTTTTT 3′];
                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female'
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares infant brain lNIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:29866"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="70 days post natal"
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6.1%;
52.0%;
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Score 53; DB 143; Length 466; Pred. No. 0 00056;
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Matches 119;

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0; Mismatches 110;

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                                                                                                                                                Matches 104: Conservative
                                                                                                                                                               Query Match 6.1%: Score 53: DB 111: Best Local Similarity 55.0%; Pred. No. 0.00059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sections
^{6/26} Aunthrecteaatghmattatategggetaetggaaceaaaattteaggaaggaataeagg 735
                                                                                            616 utgatacetaggateceagagtggetgtttgtggeeagttactacatggegtatttcaae 675
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                                           20 ATGGCAGACAAGATCCCCAACTGGGTTTATCTTGCAGCTTACITTATAGCCTACTTCAAT 79
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Plate: 74 row: F column: 15
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onpublished (2000)
Contact: Smith TPL
USIN, ARS, US Meat Animal Research Center
PO Rox 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith*email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 402 762 4366
Fax: 402 762 4390
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Smith.T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Hennett.G.A., Fahrenkruu,S.C., Freking,B.A., Rohrer,G.A., Laegreid,
W.W. and Keele,J.W.
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RE668896.1 GI:10029487
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159318 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
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Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                /note-"Vector: pCMV SPORTS: Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from day 20 and day 40 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab_host="DH10B"
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566
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Db 80 AGCTGAGATG 208

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80 AGCTGAGATG 208
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Search completed: February 18, 2001, 23:47:34 Job time: 15998 sec

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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     February 18, 2001, 15-45-08
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Gapop 10.0 , Gapext 0.5
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1514
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match
/ cgn2_2/gcgdata/genesed/genesedp/AA1992.DAT: *
/cgn2_2/gcgdata/genesed/genesedp/AA1992.DAT: *
/cyn2_2/gcgdata/genesed/genesedp/AA1992.DAT: *
/cyn2_2/gcgdata/genesedy/genesedp/AA1994.DAT: *
/cgn2_2/gcgdata/genesed/genesedp/AA1995.DAT: *
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2/gcdd3t=//eneseq//
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Domain

Human mu opioid re	R71966	16	400	17.0	257.5	4.5
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A murine mu-opio	5	2	202	17 0	J t	1
nsus mumar	27	18	380	17.0	21)
and or proce	95	20	370	17.0	258	41
uman Cantotain	97	20	370	17.0	258	40
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G protein-	1	17	370	17.0	N	ယ္ထ
uman pituitary	ά	2	444	17.1	5	37
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murine muropic	č	21	409	17.1	258.5	ပ
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murine mu-opi	σ	N	390	17.1	58	31
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n neurop) C	420	18.3	7.	18
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creas	000	17	348	18.4	279	Ç,
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mun gurumran rece	20	17	349	18.8	285	ω̈
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ALIGNMENTS

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UP TO THE TENT TO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High-affinity melatonin-la receptor fragment.
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61..85
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42..60
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28..41
                                                                              /note= "Intracellular loop"
66..71
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                                           "Futative cytochrome-c family heme binding site"
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Best Local :
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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                        The sequence represents a fradment of a human high-affinity molatonin-la receptor, which is a membrane protein, coupled to quantine nucleotide binding proteins (6-proteins), with 7 hydrophobic putative transmembrane domains. The full-length sequence is given in RB812. Receptor fragments which interact with molatonin, or specific antibodies, may be used as receptor adomists or receptor-antagonists. Appnists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic unimal for use as a model system to screen agenists and antagonists.
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121
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                                                                                                                                                                                       Local Similarity
                                                                                                                                             1 GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
                                                                     AINPYCYTCHSLKCDKLYSSKNSLCYVLLTWLLTAAVLPNLKRGTLGYEPKTYSCTFAGS 120
                              VSSAYTIAVVVEHELVEMIIVIFCYLFIWILVLQVPQPVKPDEKPKLKPHDEBNEVIMEV 180
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                                                                                                                                                                                                                                                 288
                                                                                                                                                                        100.0%; Score 1514; DB 17, midrity 100.0%; Fred No 2.4e-159; Conservative 0; Mismatches 0;
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940S-0261857.
940S-0319887.
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213..234
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229..233
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202..2
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177..2
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154..1
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105..125
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64..88
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62..67
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52..63
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147...1
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28..51
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215..23
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263..2
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127..13
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                                                                "Intracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Conserved melatemin receptor motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Extracellular domain"
                                                                                                              "Conserved melatomin receptor-la motif"
                                                                                                                                                         "Transmembrane region-VII"
                                                                                                                                                                                                        "Extracellular loop"
                                                                                                                                                                                                                                                    "Transmembrane region-VI"
                                                                                                                                                                                                                                                                                               "Intracellular lcop"
                                                                                                                                                                                                                                                                                                                                          "Transmembrane region-V"
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transmembrane region-IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Intracellular loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Extracellular long"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Intracellular loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Transmembrane region-I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Putative cytochrome-e family heme binding site"
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XDXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1994;
07-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor-agonists or receptor antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night eyels disorders, to central ovulsation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 putative transmembrane domains. A partial sequence is given in R88411. The N-terminus contains 2 consensus N-glycosylation sites, compared to 1 site in the Xenopus receptor (R88409), and the C-terminal tail is 65 amino acids shorter. Receptor fragments which interact with melatunin, or specific antibodies, may be used as reconstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor, which is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins), with 7 hydrophobic nucleotide binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 5; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T09950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MASS-) MASSACHUSETTS GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a human high-affinity melatonin-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                       W15786:
                                                                                           W15786 standard: Protein: 350 AA
                 23-JUN-1997
                                                                                                                                                                                   302 frkeyrriivslctarvffvdssndvadrvkwkpsplmtnnnvvkvdsv 350
                                                                                                                                                                                                                       240 FEKEYPPIIVSLVTARVFFVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 288
                                                                                                                                                                                                                                                         242 vvfvlfaicwaplnfiqlavasdpasmvpripewlfvasyymayfnsclnaiiygllnqn
                                                                                                                                                                                                                                                                                                                                                                                                                                61 AINPYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 unifveslavadlevalypyplelmsifnngwnlgylhcgesaflmalseigsifnitgi 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GNIEVVSLAVADLVVAIYPYPLVLMSIENNGWNLGYLHCQVSGFLMGLSVIGSIENITGI 60
                                                                                                                                                                                                                                                                                                                                                                                                            ainrycyichslkydklyssknslcyvlliwlltlaavlpnlragtlqydpriysctfaq 181
                                                                                                                                                                                                                                                                                                                                    SVSSAYTIAVVVEHELVPMIIVIECYLRIWILVLQVRQPVKPDRKPKLKPHDERNEVTME 179
                                                                                                                                                                                                                                                                                                VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIISGYWNQN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                 (first entry)
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94US-0319887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.3%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1443.5; DB 1/; Lung-
Fred, No. 2.2e-152;
Fred, No. 2.7: Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Melatonin receptor protein; human; chinese hamster ovary cell; CHO cell; jet lag; sleeplessness, seasonal melancholia; Alzheimer's disease; dementia; cerebral thrombosis; high blood pressure; cancer; melancholia; ovulation regulator, neurosis; mental confusion; glaucoma; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the human melatonin receptor protein. The DNA encoding this sequence is used in an expression vector designated pakkor-hweir? The expression vector is used to produce the chinese hamster ovary (CHO) cells of the invention. The CHO cells express the human melatonin receptor protein, and can be used to identify compounds (such as agonists and antagorists) having affinity to the receptor. The CHO cells can also be used to produce the receptor. The melatonin receptor agonist can be used as an agent for preventing or treating jeting, steeplessness, seasonal melancholia, Alzheimer's disease, dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melatonin receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP09084581-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iag, sleepiessness, seasonal melancholia, Alzheimer's disease, commencial caused by cerebral thrombosis, various diseases accompanying ageing, high blood pressure, cancer, and glaucoma. The melaturin receptor antagonist can be used as an ovulation regulator. The melatonin receptor antagonist can be used as an agent for preventing or treating melancholia, neurosis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 16; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant human melatonin receptor protein and (ant)agonists used for treating jet lag, Alzheimer's disease, melancholia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T60593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mental confusion.
302 frkeyrriivslotarvffvdssndvadrvkwkpsplmtnonvvVvdsv 350
                                           240 FRKEYFFIIVSLVTAFVFFVDSSNDVADRVKWKESPLMINNNVVKVDSV 288
                                                                                      242\ vvfvlfaicwaplnfiglavasdpasmvpripcwlfvasyymayfnsclnaiiygllnqn
                                                                                                                                                                               182 svssaytiavvvfhflvpmııvifcylriwilvlqvrqrvkpdrkpklkpqdfrnfvtmf 241
                                                                                                                                                                                                                          120 SVSSAYTIAVVVFHELVPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDFRNFVTMF 179
                                                                                                                                                                                                                                                                                                                 61 ATHRYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPHLRRGTLOYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                            62 gnifvvslavadlvvaiypyplvlmsifnngwnlgylhcqveqflmglsvigsifnitgi 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                      ainrycyichsikydkiysskasicyvlliwiltiaavlpniragtigydpriysctfag 181
                                                                                                                                                                                                                                                                                                                                                                                                        GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
                                                                                                                                 VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAJISGYWNQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.38;
96.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1443.5; DB 18; Length 350; Fred. No. 2.2c-152; 1; Mismatches 7; Indels 1;
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                                                                                                                                                                                                                                                                                     Best Local Sir
Matches 278;
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This represents a human melatonin receptor mel-la. The invention provides materials for screening for a substance showing affinity for a melatonin receptor protein, which comprises an animal cell containing an expression plasmid for the gene encoding a human melatonin receptor protein. The cells are useful for screening for human melatonin receptor proteins and its agonist or antagonist e.g. hormones and synthetic proteins and its aconist or antagonist e.g. hormones are combinent.
                                                                                                                                                                                                                                                                                                                                                                                                       hyman melatodic receptor protein is useful as it has the same activity natural human melatodic receptor protein. The new screening method is better than prior att radioimmunoassay techniques at quantitatively determining melatonic, which uses antibodies produced by linking melatonic to a carrier.
                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples: Fig 2: 24pp: English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koda J. Shirono H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JCRP-) JCR PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melatonin receptor: mel-la;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human melatonin receptor protein mel-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W94761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human melatonin receptor proteins and admists and antagenists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New melatonin-receptor expression cells - useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 1999-083563/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compounds by measuring changes in metabolic activity. The recombin-
human melatudin receptur frutein is useful as it has the same aptiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-1999
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              12
42
13
                                             180 VVFVLFAIGWAPLNFIGLAVASDPASMVPKIPEWLFVASYYMAYFNSCLNAIISGYWNQN 239
                                                                                                              20 SVSSAYTTAVVVEHELVPMITVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDERNEVTME 179
                                                                                                                                                                                61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                   | GNIFYVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHOQVSGFLMGLSVIGSIFNITGI 60
vefelfafewaplofiqiavasdpasmepripqwifeasyymayfosoloaliyalloqo
                                                                             svssaytiavvvfhflupmiivifcylriwilvlqurqrvkpdrkpklkpqdfrnfutmf 241
                                                                                                                                                ainrycyichslkydklysskosleyvlliwlltlaavlpolragtlqydpriysotfaq läl
                                                                                                                                                                                                                    qnitvvslaradivraiypypivlmsifnngwnlgylhogrsgflmglsrigsifnitgi 121
                                                                                                                                                                                                                                                                                     Similarity 96.78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          350 AA;
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                                                                                                                                                                                                                                                                                                      94.9%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yokoyana
                                                                                                                                                                                                                                                                                    Score 1436.5; DB
Pred. No. 1.3e-151
2; Mismatches 8
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                                                                                                                                                                                                                                                                                                                        DB 20; Length 350;
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                        Nucleic acid comprising melatonin la receptor promoter and reporter gene - used to transform cells for screening for agents that alter transcription from promoter, e.g. for correcting circadian rhythm
                                                                                       Reppert SM;
                                                                                                                                                                                  W09803549-A1
                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melatonin la receptor, Mella gene, dirodian rhythm; puberty; reproductive cycle; jet lag; mouse; Geprotein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse melatonin la receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w23958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W23958 standard.
                                                             N-PSDB; V04644.
                                                                                                        (GEHO ) GEN HOSPITAL CORP
                                                                                                                            18-JUL-1996;
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                                                                                                                                                                29-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                               97W0-US12526
                                                                                                                                                                                                                                                                                                                       /note= "Ser is O-phosphorylated"
143 145
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Asn is N-glycosylated" 10...12
                                                                                                                                                                                                                             /label= VI
/note= "transmembrane region VI"
                                                                                                                                                                                                                                                                                                       /note=
150 .1
                                                                                                                                                                                                                                                                                                                                          135..137
                                                                                                                                                                                                                                                                                                                                                 /label= III
/hote= "transmembrane region III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein, 353
                                                                                                                                                                                                    /note= "transmembrane region VII"
                                                                                                                                                                                                                                                        /note= "transmembrane region V"
                                                                                                                                                                                                                                                                                   /label= IV
/note= "transmembrane region IV"
                                                                                                                                                                                                                                                                                                                                                                                     /label= II
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "tiansmembrane region I"
                                                                                                                                                                                                                                                                                                                                                                                                                /label= I
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Asn is N-glycosylated"
                                                                                                                                                                                                             /label= VII
                                                                                                                                                                                                                                                                  /label= V
                                                                                                                                                                                                                                                                                                                                                                            /note= "transmembrane region II"
                                                                                                                                                                                                                       . 298
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                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                              "Ser is O-phosphorylated"
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disorders or controlling reproduction in animals

45μp; English

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    R88413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This protein comprises the mouse melatonin la (Mella) receptor, a G-protein coupled receptor that specifically binds melatonin and signals the melatonin-mediated cascade of biological events. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to alter transcription from the promoter (claimed) (A) that are activators are useful for treating circadian rhythm disorders in humans (e.g. jet lag. Sleep-wake disturbances in the blind or regulation of ovarian cyclicity ) and for control of the reproductive cycle in seasonally breeding animals, while those that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claimed nucleic acid (I) comprises a functional melatonin la receptor gene promoter (see V04644) linked to a reporter gene.
06-JUN-1995;
17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are inhibitors are used to control initiation and timing of puberty in humans. Screening for (A) can now be done in cultures of transformed cells which do not naturally express the receptor (which is naturally localised to a few specific sites in the central nervous
                                                                                                                                                                                                                                                                              Melatonin-la receptor; mouse; 3-protein-coupled receptor; melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-laq; day-night cycle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R88413 standard; Protein; 353
                                                                                                                                                                                                                                          ovulation: reproductive cycle; animal breedi antibody; transgenic animal; drug screening.
                                                                                                                                                                                                                                                                                                                                                                High-affinity melatonin-la receptor.
                                                                               07-JUN-1995;
                                                                                                                          28-DEC-1995
                                                                                                                                                                 W09535320-A1
                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 svssaytiavvvíhřivpmiivifcylriwvlvlqvrrrvkpdnkpklkpqdfrnfvtmf 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVSSAYTIAVVVEHELVPMIIVIECYLRIWILVLQVPQPVKPDRKPKLKPHDFRNEVTME 179
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    94US-0251857
94US-0319887
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                                                                                   95WO-US07360
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Best Local Similarity
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                                                                     day-night cycle disorder; ovulation, reproductive cycle; antibody; animal breeding; puberty; transgenic animal; drug screening.
                                                                                           Melatonin-la receptor; sheep; G-protein-coupled receptor; cytochrome-c family heme binding site; melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovuiation, reproductive cycle; antibody;
                                                                                                                                                                                                 High-affinity melatonin-la receptor.
                                                                                                                                                                                                                                                                                    R88410;
                                                                                                                                                                                                                                                                                                                        R88410 standard; Protein; 366
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.4%, Score 1292.5; PB 17; Length 353;
83.7%; Pred. No. 1.4e-135;
Live 24; Mismatches 22; Indels 1;
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05-JUN-1995;
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07-OCT-1994;
         receptor, which is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins), which Thydrophobic putative transmembrane domains. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agenists or receptor-antagonists. Agenists may be used in therapy of circulain rhythm disorders such as jet-lag or day-night cycle disorders, to control evulation, or in alteration of
                                                                                                          Claim 6; Fig 2: 115pp; English.
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receptor agonists or antagonists e.g. for regulating circadian
rhythm disorders or reproductive cycles
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                                                                                      The sequence represents a sheep high-affinity melatonin-la
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eyeles in seasonally breeding animals
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44..68
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23..25
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105..1
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78..83
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Pred. No. 6.8e-130;
Wismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences W25926-7 represent novel illelic Xenopus laevis melatonin receptor MEL-IA proteins. This sequence is a new form of the melatonin receptor designated MEL-IAA, also known as Mel 1-c(alpha). The protein differs from previously known receptors by being 65 amino acids shorter and also having 2 different C-terminal amino acids. The protein is encoded by 2 different alleles (T70063-4) which differ in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mBNA. The coding sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T7067-76. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signalling. MEL-IAA has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular scene house the same protein of the protein sequence and transmembrane inhibit adenylyl cyclase, but both proteins can modulate intracellular scene and the same protein of the protein sequence and the same protein that the same protein inhibitor of the same protein inhibitor of the protein sequence and the same protein that the same protein is the same protein of the same protein inhibitor of the same protein is a new form the same protein sequence and the same protein is the same protein in the same protein in the same protein is the same protein in the same protein in the same protein is the same protein in the same protein in the same protein in the same protein is the same protein in the same protein in the same protein in the same protein in the same protein is the same protein in the same protei
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                                                     EPKEYPRIIVSLVTARVFEVDSSNOVADBVKWKPSPLMTNNN 281
                                                                                                                                                                                                                                                                                 SVSSAYTIAVVVEHELVEMIIVIEGYLEIWILVLQVEQEVKEDEKEKLKEHDERNEVTME 179
                                                                                                                                                                                                                                                                                                                                                                                          AINRYCYICHSLKCEKLYSSKNSLCYVLLIMLLE-AAVLPNLREGTLEYEPRIYSCTFAE 119
                                                                                                           vvfvlfavowaplnfiglavainpfhvapkipewlfvlsyfmayfnsclnaviygvlngn
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; Pred. No. 1.1e-109;
49; Mismatches 42;
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                        "Intracellular domain'
                                                                      "Conserved melatonin receptor-ib motif"
                                                                                                                 "Transmembrane region-VII"
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Best Local
                                                                                                                                                                                                                                                                                                                                                             melatonin, or specific antibodies, may be used as receptor agonists or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally branding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   form of a ligand binding pocket. Phosphorylation sites in the C-tail may be involved in receptor regulation. Primers from the encoding DNA may be used for isolation of sheep, mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           form a stabilizing disulfide bond. Pro residues in transmembrane domains IV, V and VI may introduce kinks in the alpha-helices to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coupled to quanine nucleotide binding proteins (G-proteins), and has 7 hydrophobic purative transmembrane domains. The N-terminus has an N-linked qlycosylation site typical for G-protein-coupled receptors, and 2 Cys residues in the 1st 2 extracellular loops may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a high-affinity melatonin receptor (mol.wt 47,424) from Xenopus laevis. The receptor is a membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5: Fig 1: 115pp; English
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07-OCT-1994;
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17-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e,g for regulating circadian
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120 SVSSAYTIAVVVFHFLVPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDFRNFVTMF 179
                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                   61 AINRYCYICHSLKCDKLYSSKNSLCYVILIWLLT-AAVLPNLPRGTLQYEPPIYSCTFAQ 119
                                                                                                                                                                                             1 GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
                                                                               ainrycyichslrydklynqrstwcylgltwiltiiaivpnffvgslgydprifsctfaq
                                                                                                                                                         qnlfvvslsiadlvvavypypviliaifqngwtlgnihcqisgflmglsvigsvfnitai 126
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                                                                                           Jockers R, Marullo S,
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Best Local Similarity
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                                                                                                                                                                            Melatonin-lb receptor human a-protein-coupled receptor; cytochrome a family heme kinding site, antibody, glycosylation melatonin receptor-advist, melatonin receptor-advist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty; transdenia animal drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulate intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike the MFL-1Aa protein, it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                             Modified-site
                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  High-affinity melatonin-1b receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R88414 standard; Protein; 362 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tvsssytitvvvvhfivplsvvtfoylriwvlviqvkhrvrqdfkgkltptdlrnfltmf 246
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A.16
Youte- "Niglynisylation site"
                                                                         Location/Qualifiers
1 40
                                                A⇔= "Extracellular domain"
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DNA encoding high affinity melatonin receptor one – used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
                                                                                                                                                                                                                              06-JUN-1995;
17-JUN-1994;
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                                                                                                                                                                         WPI: 1996-058368/06
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9408-0261857
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/note=
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77..101
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309..36
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277..2
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1362
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                                                                                                                                                                                                                                                                                                                "Conserved melatonin receptor la motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Transmembrane region-II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conserved melatonin receptor motif"
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                                                                                                                                                                                                                                                                                                                                                                           "Intracellular loop"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     "Putative cytochrome-e family heme binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Intracellular loop"
                                                                                                                                                                                                                                                                                                                              "Iransmembrane region-VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                       site"
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transmembrane domain, and an NAXXY motif in transmembrane-7, rather than NPXXY. A CYILMS motif, which is a consensus site for cytochrome-o family beme binding, is present in both lb and la-type receptors. The N-terminus contains I consensus N-glycosylation site, Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-altagonists. Agonists may be used in therapy of circadian rhythm discribers such as jet-ing or lay-hight cycle discribers, to condition ovulation, or in alteration of reproductive cycles in swasonally breading animals. Autagonists may be used to control the

The sequence represents a novel human high-affinity melatonin-1b receptor (mol wt. 40,188), which is a membrane protein, coupled to quantife nucleotide kinding proteins (6 proteins), with 7 bydrophobic putative transmembrane domains. Single features of 1b receptors include an NRY motif downstream from the 3rd transmembrane with the 3rd transmembrane from the 3rd transme

Claim 10; Fig 6; 115pp; English.

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Calininergic receptors are useful as biological and pharmocological research tools and for production of antibodies. Agonists of such receptors are useful as analgesics. Probes directed against the game are useful for detecting expression of galaninergic receptors, for defecting generalities, for diagnosing neurological,
                                                                                                                Claim 8; Page 15-18; 27pp; French.
                                                                                                                                                 New galanin receptor gene - useful for diagnosing neurological, cardiovascular, endocrine or psychiatric disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calanin receptor; gene; antibody; analgesic; probe; detection; diagnosis; neurological disorder; endocrine disorder, psychlatric disorder, gene expression; ds.
                                                                                                                                                                                                          N-PSDB; 097304
                                                                                                                                                                                                                                                                                                                                     17-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galanin receptor
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                                                                                                                                                                                                                                                                                                 (RHON ) RHONE POTTENC RORFR SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system
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                                                                                                                                                                                                                            1995-285172/38.
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Matches 76; Conserv
                                                                                                                                                                                                                                                                                              31-MAY-1995;
13-OCT-1994;
28-DEC-1994;
                                              Claim 1; Page 48-50; 71pp; English.
                                                                                    diabetes or dementia
                                                                                              Isolated galanin receptor proteins - used partic. to identify agonists or antagonists, which can be used to treat, e.g. ulcers.
                                                                                                                                                         N-PSDB; T29436
                                                                                                                                                                      WPI: 1995-232095/24.
                                                                                                                                                                                                           Ohtaki T,
                                                                                                                                                                                                                             Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galanin receptor, stomach ulcer; antiulcer; diabetes; antidiabetic; dementia; neuropeptide: sedative: Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human galanin receptor.
                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-1996
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                                                                                                                                                                                                                           Fukusumi S,
                                                                                                                                                                                                           Onda H;
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94JP-0247599.
94JP-0325610.
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26.3%; Pred. No. 1.5e-23;
ative 62; Mismatches 129,
                                                                                                                                                                                                                         Hinuma S,
                                                                                                                                                                                                                       Hosoya M, Ohgi K;
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This sequence encoding a human galanin receptor protein may expressed recombinantly in e g \mbox{CHO} cells. This protein is

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              particularly used to identify admists or antagonists which can be used to treat e.g. where, dishertes or dementia, etc. The protein can also be used for the detection of galanin, in the production of antibodies, and transgenic animals.
The present invention describes peptides (1) binding to galanin r proteins (1) contain the sequence APAHPGPGG or one substantially
                                                Claim 1: Page 119-121: 153pp; Japanese
                                                                               Peptides binding to galamin receptor kidney functioning -
                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                 25-MAR-1448.
21-SEP-1998.
                                                                                                                                                                                                                                                                                                  24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                 40-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                  W09948920-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                function regulator; prostate; testis; skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Physiologically active poptide; receptor binding; galanin receptor; GALP1: GALP2: GALP3: chymotrypsin; ligand; preprogalanin; galanin; drug devolopment; memory function; appetite improver; womb; kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat dalanin receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y45129 standard: Protein; 346 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 VIMEVVEVLEALGWAPLNEIGI -----AVASIPASMVPRIPEWLEVASYYMAYENSCLNA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y match 18.8%; Score 285; DB 17; Local Similarity 26.3%; pred. No. 1.5e-23; hes 75; Conservative 77; Minmatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                 1999-572170/48
CB; Z25518.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtvlvvvvvfgiskipbhiiblkanfgvfpl-pasflfri----tabolayeresmp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vdryvaivhsrrssslrvsrnallgvgciwalsiamaspvayhqqlfhprasnqtfcweq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nlfilnlsiadlayllfcipfqatvyalp+wvlgafickfihyfftvsmlvsiftlaans 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SSAYTIAVVVEHELVEMIIVIFCYLFIWILVLQVPQPVKFDFKFKLKEHDFBNF
                                                                                                                                                                                Matsui H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                   98JP-0266972
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                                                                                                                                                                                 Ishibashi Y.
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                                                                                                                                                                                egi K.
                                                                                               proteins, used
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-1995;
13-OCT-1994;
28-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identical to it, and their precursors, salts, andes and esters, which bind especially to rat galacia receptor protectors. Products from the present invention are used in assays of galacia by ideal and receptor binding and the development of drugs acting on galania hading, such as memory function improvers, appetite improvers, and function requiators for the womb, kidney, prostate, testis or skeletal muscle. Yallya to yasia and resistent process and function in the companion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galanin receptor: stomach ulcer: antiulcer: diabetes; antidiabetic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse pancreas beta-cell line MIN6 galanin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R95069 standard, Protein. 348
      ciabetes or dementia
                                  Isolated galanin receptor proteins - used partic, to identify againsts or antagenists, which can be used to treat, e.g. ulc
                                                                                                                                      N-PSDB; T29435.
                                                                                                                                                                                                                                                                  Fujii k,
                                                                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :1-00T-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 FRNEVIMEVVSVLEALGWASLNEIGL · · · · AVASDEASMVESISEWLSVASKYMAKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 rdiyrairheiiseSlireinallgrafiwalsiam -
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Local Similarity 28.0%, Pred. No. 4.1e-23;
hes 73; Conservative 57; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 INPYOYIOHSLKODKLYSSKNSLOYVLLIWILTAAVI.PNI PPOTLOYEDRIY----SCIF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                              Fukusumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuropeptide; sedative;
                                                                                                                                                                                                                                   Onda H;
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94JP-0326610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encoding a mouse galanin receptor protein was obtained from the mouse pancreatic beta-cell line, MIN6 (FERM BP-4954), and may be expressed recombinantly in eq. CHO cells. This protein is particularly used to identify agonists or antagonists which can be used to treat e.g. ulcers, diabetes or dementia, etc. The protein can also be used for the detection of galanin, in the production of antibodies, and transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 46; 71pp; English.
                                                                                                                                                                                                                                                                       131 vdryvaivhsrrssslrvsrnallqvqfiwalsiam----aspvayhqrlfhrdsnqtf 185
                                                                                       242 kktartvlvvvvfqiswlphhvvhlwaefqafpltpasfffri-----tahclaysns 295
                                                                                                                                 172 FRNFVIMEVVEVLEAICWAPLNFIGL---- AVASDPASMVPRIPEWLEVASYYMAYENS 226
                                                                                                                                                                                  296 svnpliyaflsenfrkaykqv 316
                                              227 CLNAIISGYWNQNFRKEYRRI 247
                                                                                                                                                                                                                             122 -----SSAYTIAVVVFHFLVPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPHD 171
                                                                                                                                                                                                                                                                                                                   52 INRYCYICHSLKCDKLYSSKNSLCYVLLIWLLTAAVLPNLFRGTLQYEPRIYSCTFAQSV 121
                                                                                                                                                                                                                                                                                                                                                                 71 nlfilnlsiadlayllfcipfqatvyalptwvlqafickfihyfftvsmlvsiftlaams 130
                                                                                                                                                                                                                                                                                                                                                                                                           2 NIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 AA;
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Search completed: February 18, 2001, 20:18:11 Job time: 12783 sec

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OM protein - protein search, using sw model
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score greater than or equal
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563.5
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1514
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Listing first 45 summaries
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/cgn2_6/ptodata/2/193/5A_COMB.pep:*
/cgn2_6/ptodata/2/193/5_COMB.pep:*
/cgn2_6/ptodata/2/193/5_CTUS_COMB.pep:*
/cgn2_6/ptodata/2/193/backfiles1.pep:*
  DB
         SUMMARIES
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(without alignments)
95.453 Million cell updates/sec
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                              sequence 4, Appli
sequence 7, Appli
sequence 8, Appli
sequence 16, Appl
sequence 9, Appli
sequence 344, App
sequence 46, Appl
sequence 46, Appli
sequence 47, Appli
sequence 3, Appli
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sequence 26, Appli
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sequence 37, Appli
sequence 37, Appli
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sequence 2, Appli
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Sequence 6, Application US/08466103A
Patent No. 5856124
                                                          US-08-466-103A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reppert, Steven M.
APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MEL
TITLE OF INVENTION: RECEPTORS AND USE
NUMBER OF SEQUENCES: 29
COPPESSEE: Fish & Pichardson P.C.
ADDRESSEE: Fish & Fichardson P.C.
STREET, 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/466.10
APPLICATION LASS
CLASSIFICATION: 435
CLASSIFICATION BATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
APPLICATION NUMBER: 07-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
APPLICATION NUMBER: 08/261,857
APPLICATION NUMBER: 08/261,857
APPLICATION TIPUTATION:
ANAME: PERSON JADIS K.
                                                                                                                                                              TELEFAX: 617/542-8906 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                               SEQUENCE CHARACTEPISTICS:
LENGTH: 288 amino acids
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CITY: Boston
                                                                                                                                                                                                                    NAME: Fraser, Janis K. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
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RECEPTORS AND USES THEREOF
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US-08-351-473B-5
US-09-170-331-5
US-07-783-602C-1
US-08-351-473B-2
US-08-16-001-6
US-08-351-473B-4
US-08-351-473B-4
US-08-351-485A-8
US-09-045-186-2
US-08-625-685A-1
US-08-525-268A-15
PCT-US93-05039-3
US-08-406-855A-21
US-08-446-734A-7
US-08-446-855A-22
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       Fied. No.
                       Score 1514,
         14, DB 2,
4.1e-126;
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Sequence 5, Appli
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Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 2, Appli
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Sequence 1, Appli
Sequence 21, Appli
Sequence 22, Appli
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                                                                 US-08-466-103A-12
Query Match
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                     NAME: FIGSEY, Janis K.
REGISTARTION NUMBER: 34,819
REFERENCE, TWANTER: 700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (1900)
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/319,887 FILING DATE: 07-00T-1994 PHIOR APPLICATION DATA: 08/211,857 FILING DATE: 17-JUN-1994 AUTORNEY/AGENT INFOPMATION:
                                                                                 HAGMENT TYPE:
                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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SOFTWARE: FastSFQ for Windows Version 2.0
CURPENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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APPLICANT: Ebisawa, Takashi
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                                                                                                                               TOPOLOGY
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225 Franklin Street
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Score 1443.5:
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                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
ORIGINAL SOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: GENES AND GENETIC MAPKERS FOR I
TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tuggle, Chrisopher K. APPLICANT: Messer, Lori A. APPLICANT: Tun-Ping, Yu
                                              ANTI-SENSE:
                                                                 HYPOTHETICAL:
                                                                                           MOLECHLE TYPE.
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 AINBYCYTCHSLKYUKLYSSKNSLCYVII IWILIIAAVI.PNLKAGILQYIPFIYSCIFAQ 181
                                                                                                                                                                                                                                                                                                               NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37.
RESERVENCE COCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 18-JU
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                                                                                                             TOPOLOGY:
                                                                                                                                       STRANDEDNESS:
                                                                                                                                                            TYPE:
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    Homo sapiens
                                                                                                             unknown
                                                                   . peptide
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                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSE2 for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                        REFERENCE/TWOKET NUMBER: 00 TELECOMMUNICATION INFORMATION: 517/542-507
                                                                                                                                                                               FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 FRKEYPRIIVSLCTARVFFVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 353
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                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                           APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                NAME: Fraser, Janis K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                    TELEFAX:
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LENGIH:
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225 Franklin Street
353 amino acids
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                                                                          617/542-890
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FastSE2 for Windows Version 2.0
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human melatonin receptor la
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REGULATORY PEGIONS AND USES THEREOF
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                                                                                                                                                  34,819
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                                                                                                                                  00786/340002
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; MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-09-280-420-2
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, Fatent No. 58561
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TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION. HIGH-AFFINITY MELATONIN
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               APPLICATION NUMBER: 08/319,887
FILING DATE: 07-0CT-1994
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                         REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION
TELEPHONE: 617/542-5070
                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34.8
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                            APPLICATION NUMBER: 08/2
FILING DATE: 17-JUN-1994
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84.4%; Fred. No. 5 1
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NAME: PRASET, Janis K.

REGISTRATION NUMBER: 14,819

REFERENCE TOOKET NIMBER: 00785/250002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 517/542-8906
TELEPAX: 617/542-8906
INFORMATION FOR SEC ID NO: 4:
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AFFILICATION NUMBER [8,7)
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                                                                                                                                                       ATTORNEY AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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225 Franklin Street
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Ebisawa, Takashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-PCS/MS-DOS
SOFTWARE: PatentTh Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORPESSONNEMCE ADDRESS:
ADDRESSEE: Zuiley, McKee, Thomic, Voorhees & Sease STREET: 801 Grand Avenue, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHAPACTERISTICS:
LENGTH: 366 amino acid
                                                                                                                                 FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heldi S.
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR TITLE OF INVENTION: PEPPODUCTIVE TRAITS IN ANIMALS NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Messer, In APPLICANT: Tun-Ping,
                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 EPAEYEKIIVSECTTKMEEVDSSUHVADEIKEKPSPITANHULIKVDSV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 ERKEYRRIIVSIVTARVEFVDSSUNDVADRVKWKPSPLMTUNUVVKVDSV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 VVFVLFAICWAPLNFIGLVVASDPASMAPRIPEWLFVASYYMAYFNSCLNAIIYGLLNQN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 VVEVLEAICWAPLNEIGLAVASDPASMVPRIPEWLFVASYYMAYENSCLNAIISGYWNQN 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 AINKYCCICHSLRYGKLYSGINSLCYVFLIWTLILVAIVENLCVGTLQYDERIYSCTETQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SYSSAYITAVYVEHELVEMLIVIEGYLKIWILVLÓVKÓKVKEDEKPKLKEHDERNEVIME 179
                                                                                       REGISTRATION NUMBER: 37,719
PEFERENCE/DOCKET NUMBER: ISURF 021591
                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER - 18-JI
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                   TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
                                                                                                                                                                                                     APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Des Moines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GNIEVVSLAVADLVVAIYPYPLVLMSIENNGWNLGYLHOQVSGELMGLSVIGSIENITGI 60
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Messer, Lori A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                          US 60/022,180
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CELL TYPE: Melanocyte US-08-896-365-7
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                  COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Twn-Ping, Yu
TITLE OF INVENTION: GENES AND GENETIC MARKERS FOP IMPROVED
TITLE OF INVENTION: PEPPOCHCTIVE TRAITS IN ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rothschild, Max F.
APPLICANT: Tuggle, Chrisopher K
APPLICANT: Messer, Lori A.
APPLICANT: Tun-Ping, Yu
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                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURPENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 VYEVLFAICWAFLNEIGLAVASDFASMVPPIPEWLFVASYYMAYFNSCLNAIISGYWNON 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 FEKEYFFITVSLVTAFVFFVDSSNDVADRVKWKESDLMINNVVKVDSV 288
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                                         FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AINEYCYICHSUKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLPRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 GNVFVVSLAVADLLVAVYPYPLALASIVNNGWSLSSLHCQLSGFLMGLSVIGSVFSITGI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 82.0%; Score 1241.5; DB 2; Length 356; Local Similarity 80.6%; Pred. No. 5e-102; es 233; Conservative 25; Mismatches 30; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       CITY: Des Moines
                                                                                                                                                                    APPLICATION NUMBER: US/08/896,365
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
NAME: Nebel, Heidi S. REGISTRATION NUMBER:
                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                       50309
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801 Grand Avenue, Suite 3200
                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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                                                                                                                                                    18-JUL-1997
                                                                  19-JUL-1996
         37,719
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; ORGANISM:
; CELL TYPE:
US-08-896-365-8
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                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application patent No. 5856124

GENERAL INFORMATION:
APPLICANT: Reppert,
APPLICANT: REPORT,
APPLICANT: RESIDENCE,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-466-103A-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
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                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER- NE-0708/466,103A FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VASEPASMAPRIPEWLEVASYYMGYENSCLNAIIYGLLNÜNERGEYRKIIVSLCTTKMFF 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 VASDEASMUPRIPEMLEVASYYMAYENSCLNAIISGYWNQNERKEYRRIIVSLUTARVFF 258
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                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                         STATE:
                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                          COUNTRY .
FILING DATE: 07-OCT-1994
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: 98/0
FILING DATE: 06-70N-1995
TASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Repport, Steven M.
APPLICANT: EDISAWA, TAKASHI
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
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REGISTRATION NUMBER: 34,819
REFERENCE/DOOKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,742-5070
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
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APPLICATION NUMBER: 08/261,857
FILLING DATE: 17-JUN-1994
AUTHORITY/AGENT INFORMATION:
                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                           COMPUTER READARLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 TVSSSYTITVVVVHFIVPLSVVTFCYLPIWVLVIQVKHPVPQDFKQKITQTDLRNFLTMF 246
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                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
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Local Similarity 67.4%; Pred. No. 6e-86;
Los 170, Conservative 49, Mismatches 42, Indels 1, Gaps
                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                        MEDIUM TYPE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
CURPENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-JUL-19
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APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Tun-ping, Yu
APPLICANT: Tuggle, Tun-ping, Yu
APPLICANT: Rothschild, Max F.
APPLICANT: Tuggle, Yu
APPLICANT: Tug
APPLICANT: Tug
APPLICANT: Tug
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/261,857
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                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAILIN3 SYSIEM: PC-LOSS/MS-LOS
SOFTWAPE: Patentin Release #1 0, Version #1.30
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             18-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513.974B
FILING DATE: 14-SEP-1945
CLASCIETTE: 14-SEP-1945
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODECULE: NO HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                     APPLICANT: Ohgi, Kazuhiró
TITLE OF INVENTION G FROTEIN COUPLED RECEPTOR PROTEIN.
TITLE OF INVENTIAL FROCCTION, AND TSE THERROF
NUMBER OF SEQUENCES: 380
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsiya
APPLICANT: Fukusumi, Shoji
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ADDRESSEE: DIKE, BRONSTEIN, PORFRTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AYTIAVVVEHELVEMIIVIFCYLRIWILVLQVRQRVKEXKKKKKHDFRNFVTMEVVEV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 515-200
TELEPHONE: 515-288-1338
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PEGISTRATION NUMBER: 37.719
PEFERENCE/DOOKFT NUMBER: ISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LFAICWAPLNFIGLAVASDPASMAPRIPEWLFV 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.8%; Score 653.5; DB 2; Length 153; Local Similarity 81.7%; Pred No 1.4m-51: hes 125; Conservative 12; Mismatch-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Sus scrofa CELL TYPE: Melanocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC YTYTCHSCHCCDXLYSSKNSI/CYVILIWILT-AAVLPNI/BPGTI/CYBPRIYSCTFAGSVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AYTIAVVVEHELVEMVIVIERYLRIWVLVLQIPWPAKPENNPRLKPQDFRNEVIMEVVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                     COUNTRY
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Hosoya, Masaki
                                                                                                                                                                                         USA
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APPLICATION NUMBER: JF
FILING DATE: 11-AUG-15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF
APPLICATION NUMBER: JF
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FILING DATE: 30-5EP-1;
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JI
FILING DATE: 30-5EP-1;
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APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-ZAN-1995
PRIOP APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA
APPLICATION NUMBER: JP 7-093989
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AFFLICATION NUMBER: IP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
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TELEPHONE: 617-523-3400
TELEFAX. 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11-AUG-1945 PRIOR APPLICATION DATA: APPLICATION NUMBER. JF 5
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LENGTH: 351 amino acids
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FILING DATE: 28-DEC-1994
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                                                                                                                                                                         191 WPDPRHKKAYVVCTFVFGYLLPLLICFCYAKV---LNHLHKKLK-NMSKKSEASKKKTA 246
                                                                                                                                                                                                                   122 ----SSAYTIAVVVEHELVPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDERNE 175
                                                                                                                                                                                                                                                             131 VDRYVAIVHSRESSSLRVSRNALLGVGCIWALSIAMASPVAYHQGLFHPRASNQTFCWEQ 190
301 IIYAFLSENFRKAYKQVFKCHIRKDSHLSDTKEN-KSRIDTPPSTNCTH 348
                                         231 IISGYWWQNFEKEYFFIIVSLVTAFVFFVDSSNDVADRVKWKPSPLMTN 279
                                                                                   247 QTVLVVVVVFGISWLPHHIIHLWAEFGVFPLTPASFLFRI-----TAHCLAYSNSSVNP 300
                                                                                                                             176 VIMEVVEVLEAICWAPLNEIGL----AVASDPASMVPRIPEWLEVASYYMAYENSCLNA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                       18.8%, Score 285; DB 3; Length 351; Local Similarity 26.3%; Pred. No. 7.2e-18; hes 76; Conservative 62; Mismatches 129; Indels 22: Gaps
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                                                                                                                                                                                                                                                                                                       62 IMRYCYICHSLKCDKLYSSKNSLCYVLLIWLLTAAVLPNLPRCTIQYEPRIYSCTFAQSV 121
                                                                                                                                                                                                                                                                                                                                                 71 NIETINISIADIAYILIECIFEQATYYALETWYLJAFTCKETHYEFTVSMLVSIFTLAAMS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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11-AUG-1994
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Rest Local
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                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/TP
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19-AUG-1995
FILING DATE: 19-AUG-1995
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0, Version #1.30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: L
FILING DATE: 16-MAR-1
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ADDRESSEE: DIKE, BRO
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APPLICANT: Fukusumi, Shoji
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APPLICANT: Fujii, Ryo
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LENGTH: 349 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: S PROTEIN COMPLED RECEPTOR PROTEIN, TITLE OF INVENTION: PROBUCTION, AND USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 SVNPIIYAFLSENFRKAYKQV 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 GWEGWENKLHKKAYVVOTEVEGYLLELLIGEGYAKV---INHIHKKIK-NMSKKSEASK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 VDBYVAIVHSBPSSSI,PVSBNALLGVGFIWALSIAM-----ASPVAYHQBI FHBDSNQTF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 FENFYTMEVVEYLFAICWAPLNEIGL·····AVASSFASMVFFISEWLFVASYYMAYFNS 226
                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/513,974B FILING DATE: 14-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 NIFILNLSIADLAYLLFCIPFQATVYALTPWVLGAFICKFIHYFFTVSMLVSIFTLAAMS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
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       16-MAR-1995
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                             JP 7-057186
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FILING DATE: 20-JAN-PRICE APPLICATION DATA: APPLICATION NUMBER:

FILING DATE:

IMBER: JP 6-326611 28-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

20-JAN-1995

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                                                       sequence 342, Application US/08513974B
Patent No. 6114139
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INFORMATION FOR SEQ IT NC: 46:
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
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AFFLICATION NUMBER: JP 6-
AFFLICATION NUMBER: JP 6-
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FILING DATE: 02-NOV-1994
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REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION
TELEPHONE: 617-523-3400
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 26.4%: Score 279: DB 3; Length 348;
Local Similarity 26.4%: prod No. 2.40-17;
hes 70: Conservative 58: Mismatches 100: ----
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Resnick, David S.
-- NUMBER: 34,235
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US:08-513-974B-342
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APPLICANT:
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APPLICANT: Ohigi, Kasuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
                                                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 342:
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APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER
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APPLICATION NUMBER:
FILING DATE: 16-MAR-
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APPLICATION NUMBER:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                          SEQUENCE CHAPACTERISTICS:
LENGTH: 348 amino acid
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                  MOLECULE TYPE:
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FILING DATE: 11-AUG-1994
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                                                                                                                                                                      NAME: Resnick, David S
RECISTRATION NUMBER: 3:
                                                                                                                                                                                                                      APPLICATION NUMBER: JF 6-189272 FILING DATE: 11-AUG-1994
                                               TYPE:
                                TOPOLOGY:
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Ohtaki, Tetsuya
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                                                            348 amino acids
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SYSTEM: PC-DOS/MS-DOS
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20-JAN-1995
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28-DEC-1994
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30-SEP-1994
                  protein
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Search completed: February 18, 2001, 16:49:53
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                                                                                                                                                                        186 CWEGWPNKLHKKAYVVCTFVFGYLLPLLLICFCYAKV---LNHLHKKLK-NMSKKSEASK 241
                                                                                                                                                                                                                                                                                                                                      | 31 VDRYVAIVHSRRSSSLRVSRNALLGVGFIWALSIAM-----ASPVAYHQRLFHRDSNQTF 185
                                                                                                 296 SVNPIIYAFLSENFRKAYKOV 316
                                                                                                                                                                                                                                                                                             122 -----SSAYTIAVVVEHELVPMIIVIFCYLRIWILVLQVEQEVKPDEKPKLKPHD 171
                                                                                                                                       227 CLNAIISGYWNONFRKEYRRI 247
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OM protein - protein search, using sw model
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                           pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Mel-la melatonin receptor - sheep c:Species: Ovis orientalis aries, Ovis ammon aries (Jamestia sheep) c:Species: Ovis orientalis aries, Ovis ammon aries (Jamestia sheep) c:paces: 19-Dec-1997 #text_change 17-Mar-2000 c:pacession: I46469 R.Repport, S.M.; Weaver, D.B.; Ebisawa, T. Neuron 13, 1177-1185, 1994

Clouing and characterization of a mammallum relatorin recoptor that mediates

A.Title:

RESULT

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ALIGNMENTS

RESULT

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A:Status: preliminary: translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-350 <RES>
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A;Title: Cloning and characterization of a mammalian melatonin receptor that mediates A;Reference number: 138848; MUID:95033233
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Mel-la melatonin receptor - human
Mel-la melatonin receptor - human
C:Species: Homo sapiens (man)
C:Species: 29-May-1998 #sequencc_revision 29-May-1998 #text_change 20-Apr-2000
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180 VVFVLFAICWAFLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCHNAIISCYWNON 239
                                                                                                                                                                                                   120 SVSSAYTIAVVVEHELVEMIIVIECYLRIWILVLQVRQPVKPDRKPKLKPHDERNEVTME 179
                                                                                                                                                                                                                                                                                                  122 AINRYCYICHSLKYDKLYSSKNSLCYVLLIWLLTLAAVULPNLRAGTLQYUPRIYSCTFAQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 95.3%; Score 1443.5; DB 2; Length 350; Local Similarity 96.9%; Pred. No. 3.9c-120; hes 280; Conservative 1; Mismatches 7; Indels 1;
                                                                                                 242 VVFVLEAICWAPLNEIGLAVASDPASMVFRIFEWLFVASYYMAYENSCLNAIIYGLLNON 301
                                                                                                                                                                                                                                                                                                                                                                                                 62 GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 121
                                                                                                                                                                                                                                                                                                                               61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLFNLPRGTLQYEPRIYSCTFAQ 119
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molatorio receptor 1b - chicken)
C:Species: Callus gallus (chicken)
C:Species: Callus gallus (chicken)
C:Species: Callus gallus (chicken)
C:Species: Callus gallus (chicken)
C:Date: 14-Feb 1997 #sequence_revision 13 Mar 1997 #text_chapge zv Apr z@w
C:Accession: S72554, S68240
R:Niznik, H.R.
Silbinitted to the EMBL Data Library, June 1995
A:Reterence number: S72554
A:Reterence in proliminary
A:Molecule type: mRNA
A:Residues: 1-289 cNIZ>
A:Status: preliminary: Manuel: Y S. Hamada:Lizaich, A., Lee, E., S., Eang, E.F., Er.W.,
A:Gross-reterences: EMBL:U30009; NID:g1050962; PID:g1050963
A:Gross-reterence number: S68240
A:Reterence number: S6
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A:Accession: 146469
A:Status: preliminary; translated from GB/EMBL/DDRJ
A:Molecule type: mPNA
A:Residues: 1-365 <REP
A:Cross-references: EMBL:014109; NID:7602131; FIDN:AAB17721.1; FID:9602132
C:Superfamily: vertebrate rhodopsin
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120 SVSSAYTIAVVVFHELVPMIIVIEOYLRIWILVLQVBQRVKPDBKPKLKPHDERNEVTMF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 Match 70.7%; Score 1070.5; DB 2; Length 289: Local Similarity 68.2%; Pred. No. 2.8e-87;
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                                                                                                                                                                                                                                                             GNAFVVSLALADLVVALYPYPLVLLAIFHNGWTLGEMHCKVSGFVMGLSVIGSIFNITAI 🚯
                                                                                                                                                                                                                                                                                                                                                GNIFVVSLAVADLVVATYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
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                                                                                  AINRYCYICHSFAYDKVYSCWNIMLYVSLIWVLIVIAIVPNFFVGSLKYDPRIYSCIFVQ 120
                                                                                                                                                                 AINEYCYICHSLECCELLYSSENSICTYULLIWILTA-AVLENILESGTIQYSEPIYSCTEAQ 119
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80.6%; Pred. No. 2.8e-102;
Vative 25; Mismatches 30;
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Exteppert. S.M.: Godson, C.: Mahle, C.D.; Weaver, D.R.: Slangenhaupt, S.A.: Gusella. From Natl And Sni 9.S.A. 92. 8734-878, 1995
A;Title: Molecular characterization of a newel molatonic receptor expressed to both A;Reference number: [38940]
A;Reference number: [38940]
A;Reference number: [38940]
A:Status preliminary: translated from GR/EMFG/DDBJ
A:Molecule type: mrNA
A:Rosidues: 1-252 FBSS
A:Cross:reterences: EMSL:025341; NID:3371133; FID::AAC50512.1; PID:0971194
C:Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                         Mellb-melatonin receptor - human
C:Species: Homo sapiens (man)
C:Pate: 31-May-1996 #sequence_revision 31-May-1996 #text_change 17-Mar-z000
C:Accession: I38990
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A, Residues 1 420 *EBI>
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C:Species: Xenopus laevis (African clawed frog)
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C;Accession: I51666
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67.4%, Fred No. 3 Ap-86,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1994
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A:Title: Cloning of a melatonin-related receptor from human pituitary A.Reference number: 870520; MUID:96228068
A:Accession: 870520
A:Status: preliminary: nucleic acid sequence not shown
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A:Residues: 1-613 <REP>
A:Cross:references: EMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Reppert, S.M., Weaver, D.R.; Ebisawa, T.; Mahle, C.D.; Kolakowski Jr., L.F. FEBS Lett. 386, 219-224, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Homo sapiens (man)
C:Date. 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S70520
melatonin receptor - striped hairy-footed hamster (fradment)
C:Species: Phodopus sungerus (striped hairy-footed hamster)
C:Date: 04-Sep:1997 #sequence_revision 07-Nov-1997 #text_change 20-Apr-2000
C:Accession: 184498
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 VVFVIFAICWAPLNCIGLAVAINPQEMAPQIPEGLFVTSYLLAYFNSCLNAIVYGLLNQN 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 LNNPVETVTIVGIHEVLPLLIVGEGYVRIWTKVLAARD - FAGQNEDNQLAEVRNELTME 240
                                                                                                                                                                                                                                                                                          240 FEKEYPPITVSLVTARVFFVDSSNDVAD 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ψ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    match 58.8%, Score 889.5; SB 2, Length 352:
Local Similarity 60.5%; Pred. No. 3.3e-71;
es 167; Conservative 45; Mismatches 63; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIISGYWNQN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TASTQYTAAVVVIHFLLPIAVVSFCYLRIWVLVLQARRKAKPESRLCLKPSDLRSFLTMF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVSSAYTIAVVVFHELVPMIIVIFCYLFIWILVIQVPQPVKPDRKPKLKPHDFBNEVIME 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AINRYCYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLPNFFVGSLEYDPRIYSCTFIQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AINRYCYICHSLKCDKLYSSKNSLCYVILIWUIT-AAVLPNIRRGTLQYEPRIYSCIFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNIFYVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
                                                                                                                                                                                                                                 FRREYWTIFHAMRHPIIFFPGLISDIRE 328
                                                                                                                                                                                                                                                                                                                                                 VIFILFAVCWCPINVLTVLVAVSPKEMAGKIPNWLYLAAYFIAYFNSCLNAVIYGILNEN 300
                                                                                                                                                                                                                                                                                                                                                                                                        VVFVLFAICWAPLNFIGLAVASDPASMVFRIPEWLFVASYYMAYFNSCLNAITSGYWNQN 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVSSAYTIAVVVEHELVEMIIVIEGYLFIWILVLQVRQPVKPDRKPKLKPHOFRNEVIME 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AINFYCYTCHSIQYERIFSVPNTCIYLVITWIMTVLAVLPNMYIGTIEYDBRTYTCIFNY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 61; Mismatches
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P:Repport. S.M.: Whaver. D.R.: Ebisawa, T. Neuron 13, 1177-1185, 1994

A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates A:Reference number: 138848; MUID:95033233

A:Accession: 184498
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A;Cross:references: EMBL:U14110; NID:g602133; PID:g602134
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Reppert, S.M.; Weaver, D.R.; Ebisawa, T.
Neuron 13, 1177-1185, 1994
A;Title: Cloning and characterization of a mammalian melatonin receptor that mediates
A;Reference number: 138848; MUID:95033233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:014409; NID:g602135; PIDN:AAA57191.1; PID-g602136 C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A,Rosidues: 1-156 /PES'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Date: 02-Aug-1996 *sequence_revision 02-Aug-1996 *text_change 20-Apt 2000 C;Accession: I62107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melatonin receptor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 FAICWAPLNFIGLIVASDPATMAPRIPEWLFVASYY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 FAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYY 220
121 FALCWAPLNFIGLIVASDPATMAPRIPEWLFVASYY 156
                                                     185 FAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYY 220
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                                                                                                                                                                   125 YTIAVVVFHFLVPMIIVIFCYLRIWILVLQVPQ®VKPÇBKPKIKPHUFRNFVTMFVVFVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YTIAVVVEHFIVEMIIVIECYLRIWILVLQVEPEVKEDSKEPIKEQDERNEVIMEVVEVL 120
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                                                                                                                                                                                                                                                           66 CYTCHSLKCDKLYSSKNSLCYVLLIMLLT-AAVLPNLKRGILGYEPRIYSCIFAQSVSSA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CYICHSLKYDRLYSNKNSLCYVFLIWVLTLVAIMPNLQTGTLQYDPRIYSCTFTQSVSSA 60
                                                                                                                61 YTIALVVEHEVVPMIIVTECYLRIWILVLQVRRRVKPDSKPKLKPQDERNEVTMEVVEVU. 120
                                                                                                                                                                                                                           1 CYICHSLKYDRIYSNKNSLCYVFLLWTLTLIAIMPNLQIGILQYDPRIYSCIFTQSVSSA 60
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             47.4%; Score 717.5; DB 2
84 6%; Pred. No. 2.3e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                           12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 156;
                                                                                                                                                                                                                                                                                                                                                 1; Gaps
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galanin receptor 1 - human C:Species: Homo sapiens (Man) C:Species: Homo sapiens (Man) C:Date 31:May-1936 #sequence_revision 31:May-1996 #**nxt_change 21:Jul-2000 C:Accession: I59386, JC5801, G01765, G02528 C:Accession: I59386, JC5801, G01765, G02528 R:Habert-Ortoli, E.: Amiranoff, B.: Loquet, I., Laburthe, M.: Mayaux, J. R:Habert-Ortoli, Sci U.S.A. 91, 9780/9783, 1994 A:Title: Molecular cloning of a functional human galanin receptor.

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A:Molecule type: mRNA
A:Possidines: 1:498 kEES*
A:Oross:reterences: EMRE:002083: NID:q403573; PIDN:AAA70049.1; PID:q403574
                                                                                                                                                                                                                                       A:Title: Characterization and distribution of a chemed rat munopioid receptor A:Reference number: 156517; MUID:95096825
A:Accession: 156517
                                                                                                                                                                                                                                                                                                                                                                                                              mu opioid receptor - rat
ClSpecies: Rattus norvegicus (Norway rat)
ClSpecies: Rattus norvegicus (Norway rat)
ClDafor 26-013[190 #soquenco_revusion 26-3ul-1996 #foxt_change 20-3un-2000
ClDafor 26-013[190 #soquenco_revusion 26-3ul-1996 #foxt_change 20-3un-2000
ClAccession, 19817, 15795], A49680, ISSS, ClS Pennekleiv, OlK.; Kelly, M.J.;
J. Neurochem, 64, 14-24, 1995
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A:Map position: 18q23-18q23
C:Superiamlly: vertebrate rhodopsin
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A:Residies: 1314, WilC-349 - EDS -
A:Residies: 1314, WilC-349 - 
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A:Residues: 1-349 <LORY
A:Cross references: GB.U53511, NIB.d1297337, FIDN.AAC51936.1, FIB.d1297338
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Biochem Biophys Res. Commun. 241, 558-564, 1997
A:Title: Cloning, chicmessmai location, and transcriptional regulation of the buman gal
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A:Accession: 159336
A:Status: preliminary; translated from GB/EMBL/DDBJ
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A:Accession: G01765
A:Status: translated from GR/EMBL/DDRI
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A:Accession: J05801
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A: Residues: 1-349 < HAB>
                                                                                                                                                                             A:Status: preliminary, translated from DR, EMBC, SCRJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 VDRYVAIVHSRRSSSLRVSRNALLGVGGIWALSIAMASPVAYHQGLFHPPASNQTFGWEQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 VTMEVVEVLEAICWAPLNFIGL-----AVASDPASMVPRIPEWLEVASYYMAYENSCLNA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [4] WPDPPHKKAYVVCTFVFGYLLPLLLICFCYAKV---LNHLHKKLK-NMSKKSEASKKKTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOL IIYAFLSENFRKAYKQVFKCHIRKDSHLSDTKEN-KSRIDTPPSTNCTH 348
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A; Gene: MUOR1
C; Superfamily:
C; Keywords - G
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A:Title: Primary structures and expression from cDNAs of rat opicid receptor deltar a A:Reference number: S34592; MUID:93351652
A:Accession: S34593
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P:Sedqi M.: Poy, S.: Pamakrishnan, S.: Elde, B.: Loh, H.H.
Ricchem Ricphys Pas Commun 200 563-574, 1945
A:Ittle: Complementary PNA olumina of a managed of receptor from rat peritoneal macro;
A:Forence number 152314, MCID:45251654
A:Accession: 152314
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C:Genetics:
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A:Molecule type: mRNA
A:Posidocs: 1:244,7V/,245,399 <THON
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A:TILLE: My uplate respector come closing and expression
A:Reference number: A48799
A:Recession: A48799
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A;Residues: 101-340 <SED>
A:Cross-references: GB:S77863; NID:g988526
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A;Title: Purification and partial amino acid sequence of a mulopioid receptor from A;Reference number: A49680; MUID:94075333
A;Accession: A49680
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A; Accession: 157951
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A. Residues 1-244, 'V', 246-398 KETTY
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B:Eppler, C.M.: Hulmes, J.D.: Wang, J.B.: Johnson, B.: Corbett, M.: Loth
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A; Pesidues: 1-398 < PE
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16 - VERYTAVCHEVKALDERTERNAKIVNVONWILSSAIGLEVMEMATTKYRQGSIDCTLTES 222
                                                                                                                                                 104 NIYLENLALAD-ALATSTLPEQSVNYLMGTWCFGTIICKIVISIDYYNMETSIETLCIMS 162
                                                                      AL INFVIXIOHECH COFCYSEKNEECYVELIMOOTAAV CHROFFOTLOVEFFIVECTFALS 120
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                                                                                                                                                                                                                            2 NIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIA 61
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                                                                                                                                                                                                                                                                                                                                       17.2%; Score 260; DB 2; 25.3%; Fred. No. 1.4e-15;
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mu opioid receptor - mouse cospectes: Mus musculus (house mouse) (C:Spectes: Mus musculus (house mouse) (C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999 (C:Date: 08-Dec.1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999 (C:Date: 08-Dec.1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999 (C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999 (C:Date: 08-Dec-1995 #text_change 24-Nov-1995 (C:Date: 08-Dec-1995 #te
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Proc. Natl Acad Sci. U.S.A. 91, 9081-9085, 1994
A.Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor A. Perference number: 148665; MUID:94377496
A: Accession: I48665
A: Status: translated from GR/EMBL/DDRJ
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A.Title: Characterization of the murine mu opioid receptor gene.
A:Reference number: A57510 MUID 95318184
A:Accession. A57510
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C:Superfamily: vertebrate rhoc
C:Keywords: alternative splic
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A; Residues: 1-398 <KA
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A:Residues: Teferences: EMBL:U10561: NID:g555696: PIDN:AAB60673.1: FID:g565069
R.Rossi .3.2. Fab. Y.X. Brown, G.F. Pasternak, G.W.
FERS Lett. 369, 192-196, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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     엉덩
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: vertebrate rhodopsin (Superfamily: derector) glycoprotein.
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:Residues: 1-398 <RO
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 PVLYAFLDENFKRCFREFCIP--TSSTIEQQNSTPVRQNTREHPS---TANTV 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 MINIBALALA ALATETEPPOSVNYLMOTWPPONILEKIVISTENYNMETSIFTLOTAS 162
                                                                                                     176 VTM-FVVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLF-VASYY----MAYFNSCLM 229
                                                                                                                                                                                                                                                                                                                                                                                                          163 VERYLAVOHEVKALDEKTERNAKIVNVENWILSSAIGUEVMENATIKYRGUSUSCILIES 222
279 TRMVLVVVAVFIVCWTPIHIYVIIKA-----LITIPETTFQTVSWHFCIALGYTNSCLN 332
                                                                                                                                                                                               223 HPTWYWENLLKICVFIFAFIMPVLIITVCY---GLMILRLKS-VRMLSGSKEKDRNLRRI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 17.1%;
Local Similarity 24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 INPRCYTCHSLKCDKLYSSKNSLCYVLLTWLLTAAV-LPNLRRGTLQYEPRIYSCTFAOS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NIFVVSLAVADLVVAIYFYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIA 61
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                                                                                                                                                                                                                                                                                                          VSSAY----TIAVVVFHFLVFMIIVIFCYLFIWILVLQVRQBVKPDBKPKLKPHDERNF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-398 <ROS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    score 258 5; DB 2; Length 398;
Pred, No. 1.9e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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C;Accession: JC7209

R;Lenz, C.; Sondergaard, L.; Grimmelikhuijzen, C.J.P.
B;Lenz, C.; Sondergaard, L.; Grimmelikhuijzen, C.J.P.
B;Cchem. Biophys. Res. Commun. 269, 91-96, 2000
A;Title: McLecular cloning and genomic organization of a novel receptor from Drosophi A;Teference number: JC7209; MUID:20160456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Julions. 98/1, 161/2, 193/2, 243/3, 282/2; 308/3; 460/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:AF220216
C:Comment: This receptor is a G-protein-coupled receptor and a tightmembrane profein
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A; Residues: 1-394 <LEN>
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C:Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A: Map position: X distal end
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                        R:Zastawny, K.L.; George, S.R.; Nguyen, T., Chong, R.; Tsatsos, J.; Briones-Orbina. R
T. Ne:rookom, 62, 2009-2105, 1994
A:Title: Cloning, characterization, and distribution of a mule; 1d 10-Ngth in rath
A:Reference number: I56504; MUID:94246380
                                                                                                                                                                                        mu opioid receptor - rat
C:Species: Battus norvegious (Norway rat).
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #coxt_change 24 Nov-1449
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A; Reference number: A; Accession: I56504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 SYYMAYFNSCLNAIISGYWNQNFRKEYRRIIVSLYTARVFFVDSSNDVADRVKW--KPSP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 PSAESEKGKERVTRMVVVVVLAFAICWLPIHVILVLKALNLYGGSHLSVI-----1QII 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 PKLKPHDERNEVTMEVVEVL--FAICWAPLNEIGLAVA-----SDPASMVPRIPEWLEVA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 TACVESTEERINSLYGFQVSFFLSSYVAPLILICFLYMGMLARLW-------KSAPGCK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -SCTEA--OSVSS--AYTIAVVVEHELVEMITVIFCYL----KIWILVLQVKQEVKSSEFF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 FDRFLAVVHPVTSMSLKTERNATLAIMCAWITIVITAIR VALSHSVETYQYHGXAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                 370 LMINQQVIK 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 LMTNNNVVK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 SHVVAYINSCINFILYAFLSDNERKAFEKVV:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match
Local Similarity 22.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NIEVVSLAVADLVVAIYFYPLVLMSIFNNCWNLGYLHCQVSGFLMGLSVIGSIFNITGIA 61
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A.Status: proliminary; translated from GR/EMRL/DDBJ A;Molecule type: mRNA A.Pesidues: 1-348 <RES>

A:Cross-references: EMBL.U35424, NID:g1C17731; Plun:AAA74186 1: PID:q1017732 C:Superfamily: vertebrate rhodopsin

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A:Molecule type: mPNA
A:Residues: 1-50, N.,52-233, V.,235-400 <WANN
R:Wang, J.B., Johnson, P.S., Persido, A.M., Hawkins, A.L., Stiffin, C.A., Uhi, S.F.
EEBS [Last, 348, 217-222, 1934
A:Title: Human mu opiate receptor, cDNA and genomic clones, pharmacologic characterizati
A:Reference number: $41075; MHID:44139428
A:Accession: $41075
    A:Map position: 6q24-6q25
C:Superfamily: vertebrate
C:Keywords: G protein comp
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N.Alternate names: MOR1 protein: opioid receptor mu
C.Species: Homo sapiens (man)
C.Date: 02-Jul-1995 #sequenco_revision 02-Jul-1996 #text_change 19-May-2000
C.Accession: 156533, A38991: $41075; $51215
R.Mestek, A.: Hurley, J.H.: Bye, L.S.: Campbell, A.D.; Chen, Y.: Tian, M.: Liu, J.: Schu
J. Neurosci. 15, 2396-2406, 1995
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A:Residues: 887-400 <BAR>
                                                                                                                                                                                                                                                                                                                                                    A:Reference number: $51215; MUID:95046336
A:Accession: $51215
                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Bare, L.A.; Mansson, E.; Yar
FEBS Lett. 354, 213-216, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A: Molecule type: mRNA
A: Residues: 1-50, 'N', 52-400 <WA2>
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A:Accession: A38991
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submitted to GenBank, August 1994
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A;Residues: 1-400 <RES>
A;Cross-references: GB:L29301; NID:q459831; PIDN:AAA73958.1; PID:q459832
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A:Title: The human mu opicid receptor: modulation of functional desensitization by calconsterence number: 156553; MUID:95198115
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                                                                                                                                                              A; Gene:
                                                                                                                                                                                          C: Gestet ins
                                                                                                                                                                                                                                                                                                        A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                         A:Title: Expression of two variants of the human mu opicid receptor mRNA in SK-N-SH col
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;Superfamily: vertebrate rhodopsin
:Knywords, G protein coupled receptor; dlycoprotein; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 NIYIFNIALAD-ALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid sequence but shown, translated from UB, EMBL, DEB.
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F)33-96/Domain, transmembrane *status predicted <TMM2>
F)407-132/Domain; transmembrane *status predicted <TMM2>
F)444-145/Domain; transmembrane *status predicted <TMM2>
F)444-145/Domain, transmembrane *status predicted <TMM4-
F)366-208/Eomain, transmembrane *status predicted <TMM4-
F)366-208/Eomain, transmembrane *status predicted <TMM6-
F)377-747/Domain, transmembrane *status predicted <TMM7-
F)377-747/F)377-747/Domain, transmembrane *status pre
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R.Bare, L.A.: Mansson, E.: Yang, D.
R.Bare, L.A.: Mansson, E.: Yang, D.
R.Bare, L.A.: Mansson, E.: Yang, D.
R.Bescription : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression of two variants of the buman mulopicid receptor menA in SK-A.Description : Expression :
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A;Residues: 387-392 <BAW>
C:Superfamily: vertebrate rhodopsin
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Artifle: Expression of two variants of the luman municipied receptor mENA in SECS-SEA, Reference number, 351215, MOID:95046336
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A.Pes.idues 1732 - RAS.
A.Cross-reteronoses EMRI.012560; NID-g607911; PIDN-AAR60354 1; PID-g507912
R:Bare, L.A.; Mansson, E.; Yang, D.
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121 VSSAY --- TIAVVVEHELVEMITVIECYLEIWILVLQVBQBVKPPBKFKIKPHDEBNE 175
                                                                                                                                                         155 VERYLAVCHEVKALDERTERNAKLINVONWILSSALGLEVMELAGIKYRÇGSILGCILIES 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 NIYIFNLALAD-ALATSILPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMS 164
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OY 176 VTM-FVVEVLFAICWAPLNEIGLAVASDPASMVPRIPEWLE-VASYY----MAYENSCLN 229

OY 176 VTM-FVVEVLFAICWAPLNEIGLAVASDPASMVPRIPEWLE-VASYY----MAYENSCLN 229

Db 281 TRAVLVVVAVFIVCWTPJHTYVIIXA-----LVTIPETTFQTVSWHFCIALGYTNSCLN 334

OY 230 AIISOYWNCNFFKEYPPIIVSLVTAPVFFVDSSNIVADRVKWKDSPLMTN 279

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Db 335 PVLYAFLDENFKRCFREFCIPISSN----IEQUNSTRIRQNTRDHPSTAN 380

Search completed: February 18, 2001, 19:20:53

Jcb time: 17052 sec
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OM protein - protein search, using sw model February 19. 2001. 13:42:23 : Search time 54.38 Seconds (without alignments) 171.032 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Computen Ltd.

Scoring table: Title: Perfect score: Sequence: Searched: US-09-226-046-6 1514 1 GNIFUYSLAVADLVVAIYPY.....VKWKPSPLMINNNVVKVDSV 288 Gapop 10.0 , Gapext 0.5 BLOSUM62 88757 segs, 32294092 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissPrct_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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014108; AB019933 AB0199332 GTF_107 GTF_107 GTF_107 GTF_107 GTF GTF_107	Transport of the party of the p	Yamada N., Toyoshima P., receptor; function and rhythm sièep disorders."; 1837(1999). **RATORIN LIKELY TO MEDIATES TONS OF MELATONIN. THE ACTIVITY STRUSSIS TOXIN SENSITIVE GUYCLASE ACTIVITY. **BRANE PROTEIN TUBEPALIS AND YECPHYSEAL FAPS TUBEPALIS AND YELPHYSEAL FARS TUBEPAL		HUMAN MILA_HUMAN MILA_HUMAN MILA_HUMAN MILA_HUMAN MILA_HUMAN MILA_HUMAN MILA_HUMAN O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 40, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) MILATONIN PROCEPTOR TYPE 1A (MEL-1A-R). MINRIA. HOMO Sapiens (Human). HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]

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                                                Mammalia;
                                                            Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster). Fukaryota: Mejazoa: Chordata: Craniata: Vertebrata: Buteleostomi;
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01: NIV: 1997 (Rel. 35, Last sequence update)
15: JUL-1998 (Rel. 36, Last annotation updat
MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).
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G_PROTEIN_RECEP_F1_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 130-285 FROM N A TISSUE-HYPOTHALAMUS, AND PITUITARY PARS TURFRALIS: MEDILINE-95033233; PubMed-7946354; Reppert S.M., Weaver D.R., Ebisawa I.; Reppert S.M., Weaver D.R., Ebisawa I.;
                                                                                                                                                                              SEQUENCE
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INTERPRO: IPP000276: -
INTERPRO: IPR002278: -
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-1: TISSUE SPECIFICITY: AT LEAST IN THE BRAIL MORE PRECISELY IN THE PARK TURERALIS AND THE SUPPACHASMATIC MUCLEUS.
-1: SIMILARLIY: BELUNGS TO FAMILY I OF G-PROTEIN COMPLED RECEPTORS.
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Submitted (NOV-1995) to the EMRL/denkank/DDBJ databases
120 SVSSAYTIAVVVEHFLVPMIIVIFÖYLRIWILVLÖVPÖRVKFFRKRKTHVEDHRNFVTMF
                       AINPYCYTCHSLKYNPLYSNKNSLCYVFLIWVLTLVAIMPNIQTGTJQVDPRIYSCTFTQ
                                           AINPYCYTCHSUKCOKLYSSKNSLCYVLLIWLLT-AAVLPNLKRGILQYEPKIYSCTFAC 11
                                                                   GNIEVVSLAIADLVVAIYPYPLVLTSIENNOMNI OYTHOOTSAFILMGI SVIGSIENITGI
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CYTOPLASMIC (POTENTIAL).
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Endocrinology 137:3469-3477 (1996).
Endocrinology 137:3469-3477 (1996).
FUNCTION, HIGH AFFINITY RECEPTOR FOR MELATONIN, LIKELY TO MEDIATES FUNCTION, THE ACTIVITY ROPERTORS OF MELATONIN, THE ACTIVITY FOR THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE GOF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE GOF THIS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

SUBCELULAR LOCATION INTEGRAL MEMBRANE PROTEIN.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Pel 35, Last annotation update)
MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).
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Q61184;
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE FS00237: G_PROTEIN_PECEP_F1_1: 1

PROSITE: FS50262: G_PROTEIN_PECEP_F1_1: 1
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PFAM; PF00001; 7tm_1;
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                                                                                                                                                                                                                                                                                                                                                                                                       PROOBS7: MELATONINR
                                                                                                                                                                                                                                                                                             coupled receptor; Transmembrane; Glycoprotein.
32 EXTRACELLULAR (POTENTIAL).
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       EXTRACELLULAR (POTENTIAL).*
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELJULAR (POTENTIAL).
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                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update
MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (CKA)
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Sioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this placement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to Ticense agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken)
Eukaryota; Metazoa: Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P49285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Melatonin receptors are for the birds: molecular analysis of receptor subtypes differentially expressed in chick brain."; Neuron 15:1003-1015(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AMNRYCYTCHSLKYDKIYSNKNSLCYVFLIWMLTLIAIMPNLQTGTLQYDPRIYSCTFTO 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- TISSUE SPECIFICITY: EXPRESSED IN OPTIC TECTUM AND RETINA, LESS IN NEOSTERATOM, HYPOTHALAMUS AND THALAMUS.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF OPPOTEIN COMPLET PECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reppert S.M., Weaver D.R., Cassone V.M., Godson C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96073557; PubMed=7576645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 FPKEYKKIIVSLCTAKMFFVESSNEEADKIKCKPSPLIPNNNLIKVDSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SVSSAYTIAVVVFHFLVPMITVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDFRNFVTMF 179
INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                         EMBL; U31820; AAA92498.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (PY SIMILARITY).
SUPCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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N-LINXED (GLCNAC ) (F
0975C2FD41B54C74 CPC64;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                 P48040; C46608;
01-FEB-1996 (Rel. 33, Created)
**O1-FEB-1996 (Rel. 33, Last sequence update)
**O1-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIAMOGR
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SEQUENCE FROM N.A.
TISSUE-PITUITARY PARS TURERALIS;
TISSUE-PITUITARY PARS TURERALIS;
MEDLINE-9503323; PubMed-7946354;
Repport S.M., Weaver D.R., Ebisawa T.,
*Cloning and characterization of a mammalian melatonin receptor that
mediates reproductive and circadian responses.";
                                                                                                                                                                                   Bovidae;
                                                                                                                                                                                                        Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Rovoidas
                                                                                                                                                                                                                                                           Ovis aries (Sheep).
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                                                                                                                                                                                                                                                                                            MTNP1A
                                                                                                                                                                                                                                                                                                              MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).
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                                                                                                                                                                                                                                                                                                                                  VARIANT
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Biochim. Biophys. Acta 1356:299-307(1997)
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THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G
PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Eukaryota; Metarca; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metarca; Chordata; Craniata; Pecora; Bovoldea
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15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Messer L.A., Wang L., Tuggle C.K., Yerle M., Chardon Womack J.E., Barendse W., Crawford A.M., Notter D.R., Rothschild M.F.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 FRQEYRKIIVSLCTTKMFFVDSSNHVADRIKRKPSPLIANHNLIKVDSV 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae: Bovinae: Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mapping of the melatonin receptor la (MTNRlA) gene in pigs, sheep, and cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97262109: PubMed=9107687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED PECEPTORS.
                                                                                                                                                                                                           G-protein coupled NON_TER 1
                                                                                                                                                                                                                                                                                                       EMBL; U73327; APGCRDB; GCR_1363;
              DISULFID
                                                                                                                                                                                                                                                                       PFAM; PF00001;
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                          PROSITE.
                                                                                                                                                                                                                                                                                  INTERPRO: IPRO00276: -
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 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVSSAYTIAVVVFHFIVPMLVVVFCYLRIWALVLQVRWKVKPDNKPKLKPQDFRNFVTMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSSAYTIAVVVFHELVPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDERNEVTMF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES
THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY PERTURSIS TOXIN SENSITIVE G
PROTEINS THAT INHIBITS ADENVLATE CYCLASE ACTIVITY.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYENSCLNAIISGYWNON 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRKEYRRIIVSI.VTARVFFVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome 8:368-370(1997)
                                                                                                                                                                                                                                                                                                    GCR
                                                                                                                                                                                                                                          PS00237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                     108654
                                                                                                                                                                                                                                                                                                                  AAC48725.1;
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    A٨
                                                                                                                                                                                                                             G_PROTEIN_RECEP_F1_1: 1: G_PROTEIN_RECEP_F1_2: 1: G_PROTEIN_RECEP_F1_2: 1: receptor: Transmembrane; Glycoprotein
                                                                                         107
128
160
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
      29370 MW:
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                                                              EXTRACELIULAR (POTENTIAL)
                                                                                                        CYTOPLASMIC
                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                EXTRACELLULAP (POTENTIAL)
                                                 CYTOPLASMIC
      DC9A675FE75ADE03 CRC54
                                                                                              (POTENTIAL
                                                                                                                          (POTENTIAL)
                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                     (POTENTIAL)
                                   SIMILARITY
                                                                                                                                                                     (POTENTIAL).
                                                 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 209;
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Best Local Similarity
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
MELATOMIN RECEPTOR TYPE 1B (MSL-1B-R) (FRAGMENT).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHICK
PROSITE; PE00001; 7tm.1: 1
PROSITE; PS00237; G_PROTEIN_PECEP_F1_1; 1.
PROSITE; PS00261; G_PROTEIN_PECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
NON_TER
1
DOMAIN
41
2
                                                                                                                                                                                                                                                                                                                                                                                           A DOVEL Chicken brain melatonin receptor.";

FEBS Lett. 374.273-278(1995).

FUNCTION. HIGH AFFINITY RESCRIPTOR FOR MELATONIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS.

THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

THOUSE SPECIFICITY: BRAIN AND KLUNEY, WITH TRACE LEVELS IN LUNGS.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ML1B_CHICK
                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a livense agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi;
Archosauria: Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pang S.F., Brown G.M., Pristupa Z.B., Niznik H.B.: "Molecular and functional characterization of a partial cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 VASDPASMVPRIPEWLEVASYYMAYENSCLNALISGYWNONFRKEYRRIIVSLVTARVFF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LVVIECYLRIWALVLQVRWRVKÞÐNKÞKLKÞQDERNFVIMEVVFVLFAICWAÐLNFIGLV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96063731; PubMed=7589552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 VDSSNDVADRVKWKPSP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 YPLVLMSIENNGWNLGYLHCQVSGELMGLSVIGSIENITGIAIRBYCYICHSLKCDKIYS 79
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 STNSLCYVELIWMLTLVAIVPNLCVGTLQYDPRIYSCTFTQSVSSAYTIAVVVFHFIVFM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 SKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQSVSSAYTIAVVVFHFLVPM 138
                                                                                                                                                                    EMBL; U30609; AAA850
HSSP; P54725; LUBA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASEPASMAPRIPEMLEVASYYMGYENSCLNALIYGLLNÜNERJEYRKTIVSLCTTKMFF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIVIECYLRIMILVLQVRQRVKPDRKPKLKPHDFRNEVTMEVVFVLFAICWAPLNFIGLA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yuan H., Sugamori K.S., Hamadanizadeh A., Lee F.J.S
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pred. No. 5.4e-70;
9; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                   MLIC_XENLA STANDARD: PPT: 420 AA. P49219, 01-FEB-1996 (Pel 33, Created) 01-FEB-1996 (Rel 33, Last sequence update) 15-JUL-1998 (Rel 33, Last sequence update) MELATONIN RECEPTOR TYPE IC (MEL-1C-R). MEDATONIN RECEPTOR TYPE IC (MEL-1C-R). Xenopus laevis (African clawed frog). Xenopus laevis (African clawed frog). Xenopus laevis (African clawed frog).
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SEQUENCE
                  between
the Euro
                                                                                                                           Xenopus dermal melanophores.";

Proc. Natl. Acad. Sci. U.S.A. 91:6133-6137(1994).

-!- FUNCTION- HIGH AFFINITY PECEPTOP FOR MELATONIN. LIKELY TO MEDIATE

-!- THE POTENT EFFECTS OF MELATONIN ON PIGMENT AGGREGATION IN

MELANOPHORES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY

PERTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ACENYLATE
                                                                                                                                                                                                                         MEDLINE-94286591; PubMed-7517042;
Ebisawa T., Karne S., Lerner M.P., Peppert S M.;
Expression cloning of a high-affinity melatonin receptor
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                          Xenopodinae: Xenopus
                                                                                                                                                                                                                                                                                                                                         Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XENLA
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ween the Swiss Institute of Bioinformatics and the EMBL outstation 
Furopean Bioinformatics Institute. There are no restrictions on it 
by non-profit institutions as long as its content is in no wa
                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN SUPPLIED SECTIORS
                                                                                                                 CYCLASE ACTIVITY
                                               SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVFVIFAFCWAPLNFIGLAVAINPSEMAPKVPEWLFIISYFMAYFNSCLNAIIYGLLNQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVEVLEATOWARTHEISTAVASOPASMVERIFEWLEVASYYMAYENSGLNAIISGYWNON 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TASSYYTIAVVVIHFIVPITVVSFCYLRIWVLVLQVPPRVKSETKPPLKPSDFFNFLTMF
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CYTOPLASMIC (POTENTIAL)
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EXTRACELULAP (FOTENTIAL)
3 (POTENTIAL).
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                                               It is produced through a collaboration
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2.8e-67;
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Best Local .
                                                                                                  P49288; P492888; P49288; P49288; P49288; P492888; P492888; P49288; P49
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SEQ"ENCE
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae: Gallus.
[1]
                                                                                   Gallus gallus (Chicken)
                                                                                                                                                                                                                                         CHICK
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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PRINTS: PRO1100; MELATONINIOP.
PROSTITE: PRO0237 (2 PROTEIN_PECEP_F1_1: 1.
PROSTITE: PSS0252: G_PROTEIN_PECEP_F1_2: 1.
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INTERPRO: IPR000276;
INTERPRO: IPR002279;
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90. Conservative
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CYTOPLASMIC (POTENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Melatonin receptors are for the birds: molecular analysis of two receptor subtypes differentially expressed in chick brain.";
Neuron 15:1003-1015(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=96073557; PubMed=7576645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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PRINTS: PRO1150: MELATONINICR.
PRONSITE: PSO0237: G_PROTEIN_RECEP_F1_1: 1.
PROSITE: PS50262: G_PROTEIN_RECEP_F1_2: 1.
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           180 VVFVLFAICWAPLNFIGLAVASDPASMVFRIPEWLFVASYYMAYFNSCLNAIISGYWNON 239
                                                                                                                           119 AINRYCYICHSLRYDKLFNLKNTCCYICLTWTLTVVAIVPNFFVGSLQYDPRIYSCTFAQ 178
                                                                                     120 SVSSAYTIAVVVFHELVPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDERNEVTME 179
                                                                                                                                                             61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                   59 GNIFVVSLSVADLVVAVYPYPLILSAIFHNGWTMGNIHCQISGFLMGLSVIGSIFNITAI 118
                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: HIGH APPINITY RECEPTOR FOR MELATONIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENTLATE CYCLASS ACTIVITY (BY SIMILARITY). SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN OPTIC TECTUM, NEOSTRIATUM, HYPOTHALAMUS, THALAMUS AND PINEAL GLAND, LESS IN CEREBELLUM AND HYPOTHALAMUS, THALAMUS AND PINEAL GLAND, LESS IN CEREBELLUM AND
                                                                                                                                                                                                                                       1 GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
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                                                   TVSTSYTITVVVVHEIVPLSIVTECYLRIWILVIQVKHPVRQDCKQKIRAADIRNELTME 238
                                                                                                                                                                                                                                                                               192;
GCR_1080
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                                                                                                                                                                                                                                                                             similarity 67.3
92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           38575 MW.
                                                                                                                                                                                                                                                                                                 69.9%; score 1058.5; DB 67.1%; pred No 2.2e-66;
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2431C474C25A8E23 CRC64:
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7 (POTENTIAL)
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic polymorphisms of human melatonin lb receptor gene in Genetic polymorphisms of human melatonin lb receptor gene in circadian rhythm sleep disorders and controls.";

Neurosci. Lett. 280:29-32(2000).

11- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTIEINS THAT INHIBITS APENYLATE CYCLASE ACTIVITY.

PROTIEINS THAT INHIBITS APENYLATE CYCLASE ACTIVITY.

11- TISSUE SPECIFICITY: EXPRESSED IN RETINA AND LESS IN BRAIN AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ebisawa T., Uchiyama M., Kajimura N., Kamei Y., Shibui K., Kim K., Kudo Y., Iwase T., Suqishita M., Jodoi T., Ikeda M., Ozeki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reppert S.M., Godson C., Mahle C.D., Wcaver D.R., Slaugenhaupt S.A., Gusella J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe T., Sekimoto M., Katoh M., Yamada N., Toyoshima R., Okawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS G
MEDLINE=20159877; PubMed=10696804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96004613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 FRKEYRFIIVSLYTARVFFVDSSNDVADRVKWKPSPLMTNNNVVKV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of a second melatonin receptor expressed in human retina and brain: the Mellb melatonin receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                          PRINTS; PRO0237; GPCRRHODOPSN.

PRINTS; PR00237; GPCRRHODOPSN.

PROSTIE; P800857; MELATONIAR.

PROSTIE; P800237; G_PROTEIN_RECEP_F1_2: 1.

PROSTIE; P850262; G_PROTEIN_RECEP_F1_2: 1.

G_PROTEIN_RECEP_F1_2: 1.

G_PROTEIN_RECEP_F1_2: 1.

EXTRACELLULAR (POTENTIAL).

TRANSMEM 43 63 1 (POTENTIAL).

TRANSMEM 43 76 CYTOPLASMIC (POTENTIAL).

TRANSMEM 64 76 CYTOPLASMIC (POTENTIAL).

TRANSMEM 77 97 2. POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCRDB; GCR_2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB033597; BAA92315.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U25341; AAC50612.1; -. EMBL; AB033598; BAA92315.1;
TRANSMEM
                                                                                                                                                                                                                                                                                                                              PFAM; PF00001;
                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPR000276; -
                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR000025; -
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                                                                                                                                                                                                                                                                                                                                                                                                                               600804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long as its content
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1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL)
EXTRACELLCUAR (POTENTIAL).
3 (POTENTIAL).
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Best Local
the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                      MELATONIN-RELATED RECEPTOR (H9).
                                                                                                                                                                                                                                                                                                                                                                                            MI.1 X_HUMAN
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                      Reppert S.M., Weaver D.R., Ebisawa T., Mahle C.D. Kolakowski L.F. Jr.;
                                                                                                                                                                                                   TISSUE+PITUITARY; MEDLINE-96228068; PubMed-8647286;
                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                        "Cloning of a melatonin wrelated receptor from human pituitary.";
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           Metazoa;
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Pred. No. 9.5e-55;
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Usage
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                                                                          MLIX_SHEEP STANDARD: PFF: 3/3 mm. 028558; 046624; 01-NOV-1997, [Rel. 35, Created) 15-DEC-1996; [Mel. 37, Last sequence update) 15-UUL-1999, [Mel. 38, Last annotation update) MELATONIN-RELETED RECEPTOR (H9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAM: PF00001: 7tml; 1.

PPINTS: PRO151: MELATONINIXP

PROSTITE: PS00237: G_PROTEIN_RECEP_F1_1: 1.

PECSITE: FS50252: G_PROTEIN_RECEP_F1_2: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (see http://www.lst
or send an email to license@isb-sib.ch).
                                               Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM: 300207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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SEQUENCE FROM N.A.
                       Bovidae; Caprinae; Ovis.
                                   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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INTERPRO: IPROC2280;
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                                                                                                                                                                                                                     301 FRREYWTIFHAMRHPIIFFPGLISDIRE 328
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                                                                                                                                                                                                                                            240 FRKEYFRIIVSLVTARVFFVDSSNDVAD 267
                                                                                                                                                                                                                                                                                               180 VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIISGYWNQN
                                                                                                                                                                                                                                                                                                                       183 LNNPVFTVTIVCIHFVLPLLIVGFCYVRIWTKVLAARD--PAGGNPDNQLAEVRNFLTMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            63 GNIFVVSLSVADMLVAIYPYPLMLHAMSIGGWDLSQLQCQMVGFITGLSVVGSIFNIVAI 122
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                                                                                                                                                                                                                                                                                                                                                                         AINRYCYICHSLOYERIFSVRNTCIYLVITWIMTVLAVLPNMYIGTIEYDPRTYTCIFNY 182
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CYTOPLASMIC (POTENTIAL)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96228068; PubMed-8647286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning of a melatonin-related receptor from human pituitary.";
FEBS Lett. 386:219-224(1996).
-i- FUNCTION: DOES NOT BIND MELATONIN (BY SIMILARITY).
-i- SUBCELLULAP LOCATION INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reppert S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM: PF00001: 7tm_1; 1.
PRINTS: PR0151; MELATONINIXR.
PR0S1TE: PS00237: G_PROTEIN_RECEP_F1_1: 1.
PR0S1TE: PS50262: G_PROTEIN_PECEP_F1_2: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The European Bioinformatics Institute. The use by non-profit institutions as long
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OMAIN 1 30 EXTRACELLULAR
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             180 VYFYLFAICWAPLNFIGLAVASDPASMYFRIPEWLFVASYYMAYFNSCLNAIISGYWNQN 239
                                                                  183 VNNPAFAVTIVCIHFVLPLLIVGFCYVKIWTKVLAARD--PAGQNPDNQJAEVRNFLIMF 240
                                                                                                                 120 SVSSAYTIAVVVEHELVPMITVIFCYLRIWILVLQVEQRVKPDPKPKLKPHDFRNEVTME 179
                                                                                                                                                                      123 AINRYCYICHSLQYERIFSVENTCIYLAVTWIMTVLAVLPNMYIGTIEYDPRTYTCIFNY 182
                                                                                                                                                                                                             61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLTA-AVLPNLRRGTLQYEPRIYSCTFAQ 119
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Best Local Similarity
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
MELATIONIN RECEPTOR TYPE IA (MEL-1A-P) (FRAGMENT).
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: AT LEAST IN THE BRAIN, MORE PRECISELY IN THE PARS TUREPALIS AND THE SUPRACHIASMATIC NUCLEUS.

PARS TUREPALIS AND THE SUPRACHIASMATIC NUCLEUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/jmn-mnca/orsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95033233; PubMed=7946354;
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FALCWAPLNFIGLIVASDPATMAPRIPEWLFVASYY 156
                                                               YTIALVVEHEVVEMIIVTECYLRIWILVLQVPPRVKPDSKPKLKPQDERNEVIMEVVEVL 120
                                                                                                YTIAVVVENE LVENIIVIECYLRIWILVLQVRQRVKPDRKPKLKPHDERNEVTMEVVEVL 184
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156 AA;
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135
                                                                                                                                                                                                                                                                                          156
18214 MW; 2B55EA40EBC6BAB1 CBC64;
                                                                                                                                                                                                                    47.4%:
                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                        Score 717.5; DB 1
Pred. No. 3.2e-43;
                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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ong as its content
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                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                            Length 156;
                                                                                                                                                                                                               Indels
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                                                                                                                                                           Matches 134;
                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            088495;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
01-001-2000 (Rel. 4
                                                                                                                                                                                                                                                          SEQUENCE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS: PRO1151; MELATONINIXR.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: AF065145: AAC21462.1; ALT_INIT. MGD: MGI:1333877; GPR50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www isb-sib ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GPR50) and mouse chromosome X (GPr50). Genomics 55:248-251(1999).
-!- FUNCTION: DOES NOT BIND MELATONIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gubitz A.K., Reppert S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99134305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryot<mark>a; M</mark>etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELATONIN-RELATED RECEPTOR (H9).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO: IPRO00276:
123 AINRYCYICHSLQYKRIFSLRNTCIYLVVTWVMTVLAVLFNMYIGTIEYDFRTYTCIFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assignment of the melatonin-related receptor to human chromosome
                                   61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLTA-AVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                           53
                                                                                                                 1 GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF 3-PROTEIN COUPLED RECEPTORS.
                                                                           GNIFVASLSVADMLVAIYPYPLMLYAMSVGGWDLSQLQCQMVGLVTGLSVVGSIFNITAI 122
                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coupled receptor;
1 30
31 51
                                                                                                                                                           Conservative
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52
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86
104
125
1144
1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
103
124
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                                                                                                                                                                                                                                                            64300 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane
                                                                                                                                                                        Pred. No. 1.5e-42
                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
: 07135000483A2425 CRC54;
                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL 7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Query Match
Best Local Similarity
Matches 126; Conserv
                                                                                   DOMAIN
NON_TER
SEQUENCE
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002781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97262109; PubMed-9107687;
Messer L.A., Wang L., Tuggle C.K., Yerle M., Chardon P.,
Womank J.E., Barendse W., Crawford A.M., Notter D.R.,
                                                                                                                                       TRANSMEM
                                                                                                                                                         DOMAIN
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                         NON
                                                                                                                                                                                                                                                                      PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE: PS50252; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                       PFAM; PF00001;
                                                                                                                                                                                                                                                                                                                                                        EMBL; U73326; AAC48726.1; -.
                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement () or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mapping of the melatonin receptor la (MTNRIA) gene in pigs, sheep, and cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Womark J.E. Bar
Rothschild M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTNR1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IS-JHL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MELATONIN RECEPTOR TYPE 1A (MEL-1A-P) (FRAGMENT).
                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                       E MAIN
                                                                                                                                                                                                                                                       G-protein
                                                                                                                                                                                                                                                                                                                   INTERPRO: IPROCO276;
INTERPRO: IPROCO345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COMPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 SVSSAYTIAVVVFHFLVPMITVIFCYLRIWILVLQVPQPVKPUPKPKLKPHDFRNEVTMF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 FRREYWTIFHAMPHPILFISHLISDI--RETWETRAL 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    m Genome 8:368-370(1997).

FUNCTION: HIGH AFFINITY PECEPTOR FOR MELATIONIN LIKELY TO THE REPROTUCTIVE AND CIMPADIAN AUTIONS OF MELATIONIN. THE POPTHIS RECEPTOR IS MEDIATED BY PERFUSSIS TOXIN SENSITIVE PROTEINS THAT INHIBITS ADENVLATE CYCLASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
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                                                                                                                                                                                                                                                     coupled receptor:
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                                                                                        154 AA;..17900 MW;
                                                                                                                      84
116
137
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40
62
83
115
136
     44.1%; Score 667.5;
81.8%; Pred. No. 8.66
tive 12; Mismatches
                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein
                                                                                                                                                     5 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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                      8.6e-40
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Indels

Gaps

Search completed. February 18, 2001, 14:36:38 Tob time: 3255 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        om protein - protein search, using sw model
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1: sp_archea:*
2: sp_bacteria
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11:
12:
13:
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1514
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               sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                              sp_bacteria:*
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                                                                                sp_phage:*
                                                                                                                                 sp_mammal:*
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sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	score	Query	Query Match Length	DB	ID	Description
,	יו הייניר	9.16	398	י ער. י	<u>045508</u>	046608 ovis aries
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n +		80.0	بر ا 80	ابر	09PT20	Q9pt20 oncorhynchu
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л 4		اد د وج		13	P87496	
5 . (ر د د ۲ ک		162	1	09PT33	Q9pt33 oncorhynchu
7	629	41.5	161	ω	Q9PT17	Q9pt17 oncorhynchu
20	J. 5.		138	ı.	047777	097777 elephas max
9	545 5		174	11	Q9JLR8	Q9jir8 rattus norv
10	355.5	CA Go	13		FT0324	STOSER mas musecula
11	277.5	18.3	420	4	Q9NR49	Q9nr49 nomo sapien
12	277.5	18.3	522	4-	Ū9¥5X5	Q'yy's home sapien
13	270.5	17.9	377	د.	C 2 4 2 4 4 5	073/33 brachydanio
14	264.5	17.5	401	11	Q9R1L9	OFILE mus musculu
15	5,63	17.4	392	л	OONK? A	
16	261.5	17.3	400	σ.	6MAM60	
17	193	17.2	78.67	תי	29W498	
18	261	17.2	392	O1	Q9NDM2	Ogndm2 drosophila
19	258.5	17.1	393	در	Q9R1M0	29rlm0 mus musculu

ALIGNMENTS

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RESULT
046638
                                                                                                                                                                                                                                Qy
                                                    Matches 233;
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   046608 PRELIMINARY; PRT; 366 AA.
046608;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MEL 1A MELATONIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                           Barrett P., Conway S., Jockers R., Strosberg A.D., Guardiola-Lemaitre B., Delagrange P., Morgan P.J.; "Cloning and functional analysis of a polymorphic variant of the ovine Mel la melatonin receptor."; Biochim. Biophys. Acta 1356:299-307(1947).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovis aries (Sheep).
                                                                                                                                          INTERPRO, IPRO00276: -.
INTERPRO, IPRO001: 7CT/18: -.
PEAM, PEOGOO1: 7CT/18: -.
PENINTS: PRO0857: MELATONINR.
PRINTS: PRO149: MELATONINIAR.
PENINTS: PRO149: MELATONINIAR.
PENINTS: PRO1037: -G. JPROFUTIN PECEPTOP: INKNOWN_1.
SEQUENCE 366 AA: 40449 MW; BA71B55FFFF5544FFF CF6764:
                                                                                                                                                                                                                                                                 Barrett P., Conway S., Morgan P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFC45219, AAC02599.1;
INTERPPO: IPP000025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97337902; PubMed=9194573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Rovoidea;
                                                                                                                                        SEÇUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
             1 GNIFVVSLAVADLVVAIYPYELVLMSIENNGWNLGYLHCQVSGELMCLSVIGSIENITGI 60
PRELIMINARY;
                                              81.0%, Score 1235.5; DB 6; Length 366;
Elarity 80.6%; Pred. No. 4.3e-97;
Conservative 23, Mismatches 30, Indols 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                Ouery Match
Rest Local :
                                                                                                                                                                                                                                                                        Rest Local Similarity
Matches 232: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO: IPR000611: ...
INTERPRO: IPR002278: ...
FFAM: PPR00001: 7tm_1: 1.
FFINTS: PR00237, GFCKKHÖDDSN.
FFINTS: PR00857; MELATONIRR.
FFINTS: PR01012; NRPEPTIDEYR.
FFINTS: FR010149; MELATONINIAR.
                                                                                                                                                                                                                                                                                                                                                                                       N'N_TER
N'N_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il-MAY-1999 (TrEMBLrel. 10, Created)
nl-mAY-1999 (TrEMBLrel. 10, Last sequence update)
nl-mAY-1999 (TrEMBLrel. 15, Last annotation update)
nl-mAY-1999 (TrEMBLrel. 15, Last annotation update)
MELATONIN RECEPTOR MELIA (FRAGMENT).
MESOCIICELUS duratus (Golden hamster).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaija: Eutheria: Rodentia; Sciurognathi; Muridae; Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gauer F., Schuster C., Poirel V.-J., Pevet P., Masson-Pevet M.; "Floning experiments and developmental expression of both melatunin receptor Mella mPNA and melatonin binding sites in the Syrian hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO: IPR000025: INTERPRO: IPR000276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brain Res. Mol Brain Pes Pri
EMBL; AF061158; AAC67241.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-SUPRACHIASMATIC NUCLEI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10036:
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                                        120 SVSSAYTTAVVVEHELVPMITVIEGYLPIWILVLQVEQEVKEDEKEKEHBEENEWIME 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLPRGTLQYEPPIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                    ۲, 7
                                                                                                                                                                                                                             1 GNIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGI 60
SVSSVYTIAVVVEHEIVPMIIVIFCYLPIMILVLCVEFPVKROSKPPLKPCTEREVTME
                                                                                      AINRYCYICHSLKYDRLYSNKNSLCYVFLIWVLTLVAIMPNLQTGTLQYDPEIXSCTFTR 176
                                                                                                                                                                                  GNIFVVSLAAADLVVAIYPYPLVLTSIFNNGWNLGYLHCQISAFLMGLSVIGSIFNITGI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROEYRKIIVSLCTTKMFFVDSSNHVADRIKRKPSPLIANRNLVKVDSV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVFVLFAICWAPLNFIGLVVASDPDSMAPRIPEWLFVASYYMAYFNSCLNAIIYGLLNQN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIISGYWNQN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AINRYCCICHSLRYGELYSGINSLCYVELIWILILVAIVPNLCVGILGYSPSIYSCIFTQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AINRYCYICHSLKCOKLYSSKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHVFYVSLAVADLLVAVYPYPLALASIVNNCWSLSSLHCQLSGFLMGLSVIGSVFSITGI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSSAYTIAVVVFHFIVPMLVVVFCYLRIWALVLQVRWKVKPDNKPKLKPQDFRNFVTMF
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325 AA:
                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                           81.5%; Score 1234.5; DB
                                                                                                                                                                                                                                                                                                                                                                                  36781 MW
                                                                                                                                                                                                                                                                             18: Mismatches
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Best Local
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INTERPRO: IPR002278: -.
PEAM; PE00001; 7tm_1: 1.
PENM; PE00001; 7tm_1: 1.
PPINTS: PR00237; GPCRPHODOPSN
PRINTS: PR00237; MELATONINR.
PFINTS: PR01149; MELATONINAP
PPINTS: PR01149; MELATONINAP
PPOSITE: PS00237; G_PPOTEIN_PEGEPTOR; UNKNOWN_1
PR0SITE: PS00436; PEFGXICASE_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mazurais D., Brierley I., Kah O., Williams L.;
"Expression of rainbow trout melatonin Receptor.";
Submitted (JUN-1999) to the EMBL/GenFank/DDBJ databases.
EMBL; AF15662; AAF00191.1;
INTERPRO: IPP00025:
INTERPRO: IPR000511:
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Eukaryota; Metazoa; Chordata; Cianiata; Vertebrata; Eutoleostoni;
Actinopterygii; Neopterygii; Teleostoi; Eutoleostoi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-001-2000 (TrEMBLIEL. 15, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MELATONIN RECEPTOR MELIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PT20
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                                                                                                                                                                                                                                                                                 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 FEKEYEFTIVSLVTARVFFVDSSNDVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 VVFVLFAICWAPLNEIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIISGYWNON 239
                                                      310 FRREYKPIVVSVCTAPIFEHGSSNDAAEPLKSKPSPLITNNNOVKLELV 358
                                                                                       240 FRKEYPRITYSLYTARVFEVDSSNOVADRVKWKPSPLMTNNNVVKVDSV 288
                                                                                                                            250 AVEVLEAVCWAPLNFIGLAVAINPEVVVPLIPEWLFVASYEMAYENSCLNAIVYGVLNQN 309
                                                                                                                                                                                                                                                                                                                  61 AINRYCYTCHSLKCUKLYSSKNSLCYVLLIWLLT-AAVLFNLEEGTLQYEFFTYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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4
                                                                                                                                                                                                                                                                           AINFYCYTCHSLKYDKLYSDKNSVGYVLLIMALIIVAIVPNLEVGSLQXGPRVYSCIFEQ 189
                                                                                                                                                                                                                                                                                                                                                       GNIEVVSLAVAGELVVALYEFEVEISIEGKSKNEGKVEGOZESGELMSVSKIGSIENITGI
                                                                                                                                                               VVFVLFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIISGYWNON 239
                                                                                                                                                                                                      SASSAYTIAVVEHELLEIMIVTYCYLEIWILVIÇVEPPVKEENPEKLIPHEVRNEVTME
                                                                                                                                                                                                                                        SVSSAYTIAVVVEHELVPMIIVIECYLRIWILVLQVEGEVKEDERFEKLKPHDERNEVTME 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEYMBLIVSLETAKMEFVDSSNEANDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 AA; 43266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%; Score 1211.5; DB 77.9%; Pred. No. 4.8e-95
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13
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               31, Indels
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   Matches 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOCKETS R., Petit L., Lacroix I., de Coppet P., Barrett P. Morgan J.P., Guardiola B., Delagrange P., Marullo S., Strosubmitted (MAR-1997) to the EMBL/GenBank/DDBJ databases. EMBL, U67880; AAB483890.1; -. EMBL, U6799; AAB48389.1; -. EMBL, U6799; AB48389.1; -.
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01.MAY.1997 (TrEMBLrel. 03. Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus idevis (African clawed frog)
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEL-1C(A) MELATONIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P87496
P87496;
                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLTel. 03, C
01-MAY-1997 (TrEMBLTel. 03, I
01-OCT 2000 (TYEMBLTEL. 15, I
MEL-10CB) MELATONIN RECEPTOR
Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P., Morgan J.P., Guardiola B., Delagrange P., Marullo S., Stros Submitted (MAR-1937) to the EMBL/Glack/CDBJ databases. EMBL, U67882, AAB48392.1: .

EMBL: U67881, AAB48391.1; ...
                                                                                                                                                                                                                                                                                       Amphibia, Batrachia: Amura: Mesobatrachia: Pipoidea: Pipidae:
                                                                                                                                                                                                                                                                                                                   Xenopus'laevis (African clawed frog)
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 AINRYCYICHSLEYDKLYNORSTWCYLGLTWILTIIAIVPNFEVGSLQYDFRIESCTFAO 186
                                                                                                                                                 TISSUE-SKIN;
                                                                                                                                                                                SEQUENCE FROM N A
                                                                                                                                                                                                                                                              Xenopodinae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 FRKEYKRILMSLLIPRLLFLDTSRGGTEGLKSKPSPAVINNN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 FRKEYRRIIVSLVTARVFFVDSSNDVADRVKWKPSPLMTNNN 281
                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 VVFVLFAVCWAPLNFIGLAVAINPFHVAPKIPEWLFVLSYFMAYFNSCLNAVIYGVLNÚN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AINRYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GNLFVVSLSIADLVVAVYPYPVILIAIFQNGWTLGNIHCQISGFLMGLSVIGSVFNITAI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVSSSYTITVVVVHFIVPLSVVTFCYLRIWVLVIQVKHRVRQDFKQKLTQTDLRNFLTMF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSSAYTIAVVVFHFLYPMIIVIFCYLRIWILVLQVRQRVKPDRKPKLKPHDFRNFVTMF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                    Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 354;
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                                                                                                         Strosberg A.D
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Best Local
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INTERPRO: IPRO00276; -.
INTERPRO: IPRO00279; -.
PPAMM: PF00001; 7tm_1; 1.
PRINTS: PRO00857; MELATONINR.
PRINTS: FR01150; MELATONINTCP.
PROSTITE, FS00227; G_PFOTE:N_PECEPTOR; UNKNOWN_1.
PROSTITE, FS00227; G_PFOTE:N_PECEPTOR; UNKNOWN_1.
             Query Match
Eest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-02T-2000 (TrEMBLrel 15, Last annotation update)
MELATONIN RECEPTOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PT33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>v</u>ýPT33
                                                                                                                                                                                                                                                                                              "Central melatonin receptors in the rainbow trout: comparative distribution of ligand binding and gene expression.";
J. Comp. Neurol. 409:313-324(1999).
                                                                                                                                                                                                                                                                                                                                                       sequence From N.A.
MEDLINF=99306591: PubMed=10379923;
Mazurais D. Brierley I., Andlade I., Drew J., Randall C., Bromage
Mazurais D., Brierley I., Andlade I., Drew J., Randall C., Bromage
Michel D., Kah O., Williams L.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 SVSSAYTIAVVVEHELVPMIIVIECYLRIWILVLQVEQEVKEDRKPKLKPHDERNEVTME 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 FRKEYRRIIVSLVTARVFFVDSSNDVADRVKWKPSPLMTNNN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 VVEVLEAVCWAPLNFIGLAVAINPLHVAPKIPEWLEVLSYEMAYENSCLMAVIYGLLNQN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 TVSSSYTITVVVVHEIVPLSVVTECYLRIWVLVIQVKHKVRQDEKQKLTEIDLENELIME 248
                                                                                                                                                                                                             INTERPRO; IPRO02278; PFAM; PF00001; 7tm_1;
                                                                                    SEQUENCE
                                                                                                                                      Receptor.
                                                                                                                                                         PRINTS; FR01149;
                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                               INTERPRO; IPR000276;
                                                                                                                                                                                                                                                                 INTERPRO; IPR000025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AINPYCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLRRGTLQYEPRIYSCTFAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GNLEVVSLSIADLVVAVYPYPVILIAIEQNGWTLGNIHCQ18GFLMGLSVIGSVENITA: 126
                                                                                                                     NON_TER
                                                                                                     NON_TER
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                                                                                                                                                                                                                                                                                Comp. Neurol. 409:313-324(1
BL; AF178929; AAD51850.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVEVLEAICWAPLNEIGLAVASDPASMVPRIPEWLEVASYYMAYENSCLNAIISGYWNON 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRKEYKRILMSLWTPRLLFLDTSRGGTEGLKSKPSPAVTNNN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189;
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                                                                                                                                                                        PR00237; GPCRRHODOPSN
PR00857; MELATONING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                        162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                           MELATONINIAR
                                                                                          18895 MW,
42.5%; Score 643.5; DB 13: 71.0%; Fred. No. 2 60:47: tive 25; Mismatches 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Mismatches
                                                                                          1E18C9151BCBAB7H CRC64;
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                                          Length 162;
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Matches 115,

Conservative

21: Indels

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%1-MAY-2000 (TrEMPLrel. 15, Last sequence update)
%1-CCT-2000 (TrEMPLrel. 15, Last sequence update)
%1-CCT-2000 (TrEMPLrel. 15, Last annotation update)
MELATONIN RECEPTOR (FRAGMENT)
%**
"incorrhynchus mykiss (Painbow trout) (Salmo qairdneri).
"incorrhynchus mykiss (Painbow trout) (Salmo qairdneri).
"Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
%*
Restaranthopterydii, Neopterydii, Teleostei, Euteleostei,
%*
Protaranthopterydii; Salmeniformes; Salmenidae; Oncorhynchus.
01 MAY-1999 (TrEMBLrel, 10, Created)
01 MAY-1999 (TrEMBLrel, 10, Last sequence update)
01-JUN-2000 (TrEMBLrel, 14, Last annotation update)
MELAFONIN RECEPTOR 1A (FRANKENT)
Elephas maximus (Indian elephant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mazurais D., Brierley I., Anglade I., Drew J., Randall C., Bromage N., Michel D., Kah O., Williams L.M.; "Pentral melatonin receptors in the rainbow trout: comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nº N. TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPGPPHQDOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEAM: PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   distribution of ligand binding and gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE-44 (05541) PubMed-10374423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFINTS: PR00857; MELATONINR
                                                                                                                                                                                                                                                                                                   185 FAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNS 226
                                                                                                                                                                                                                                                                                                                                                                                               125 YTIAVVVEHELVEMIIVIECYLEIWILVLQVEQEVKEDEKEKKEHDEENEVTMEVVEVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTERPRO: IPR000025:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                          121 FAVOWAPLNFIGLAVAINPREGV-NIPEWEFTASYFMAYFNS 161
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                                                                                                                                                                                                                                                                                                                                                 61 YTTTVVVVHFTLPISIVTYGYLRIWILVLQVBBBVKPDTBBKIKPHDFHTFTTMEVVFVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 CYTCHSLKCDKLYSSKNSLCYVLLIWLLTA-AVLPNLRRGTLQYEPRIYSCTFAQSVSSA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAICWAPLNFIGLAVAIDPETVAPRIPEWLFVVSYFMAYENS 162
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AF178538; AAD54384.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity 71 (
): Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
161 M:
                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.5%; score 629;
71.0%; Pred No 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred No 4 4e-46;
                                                                                                                                         PRT;
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                                                                                                                                         138 AA
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Best Local Similarity
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Best Local Similarity 81.6
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                            OSJILR8:
01-027-2000 (TrEMBLrel 15, Greated)
01-027-2000 (TrEMBLrel 15, Last sequence update)
01-027-2000 (TrEMBLrel 15, Last annotation update)
MT2_MELATONIN_RECEPTOR MEL-1E (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPR000025; -.
INTERPPO; IPP000276; -.
INTERPRO; IPR002278; -.
PFAM; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; NCFI_TaxID=10116;
                                                                                                                                        SEQUENCE
                                                                                                                                                                                   Receptor.
                                                                                                                                                                                                    EMBL; AF141863; AAF66601.1;
                                                                                                                                                                                                                  "Rat MT2 melatonin receptor partial cDNA.";
Submitted (APR-1999) to the EMBL/GenBank/DDB1 databases
                                                                                                                                                                                                                                                   Poire! V J
                                                                                                                                                                                                                                                                STRAIN-WISTAR,
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         Rattus norvegious (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09JLR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00237; GPCREHOLOPSN. PRINTS; PR00857; MELATONINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Elavsky N.E., Ernst C.W., Messer E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eurberia: Proboscidea; Elephantidae, Elephas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 FIGLAVASDPASMVPR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 FLVPMIIVIFCYLRIWILVLQVPQPVKPDRKPKLKPHDFRNEVIMEVVFVLFAICWAPLN 193
                              55 YOYICHSEKCEKEYSSKNSECYVELIWEET-AAVEFNEFFGILGYSFFIYSCIFAQSVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 FIVPMIIVIFCYLRIWVLVLQVBWBVKPDNKTKLKPQDFRNEVTMEVVEVLFAICWAPLN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 DKLYSSKNSLCYVLLIW-LLTAAVLPNLREGTLQYEPRIYSCTFAQSVSSAYTIAVVVEH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EKLYSNKNSLCYVELIWVLMLVAIVPNLCTGILQYDSKIYSCTETRTVSSAYMIAVVVEH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
YWCICHSATYHRACSOWHAPLYISLIWIATIVALVPNEEVGSLEYDPKIYSCTFIQTASI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGLVVSLDPASMVPR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 AA;
                                                                                                                                        174 AA;
                                                                                                                                                                                                                                                 , Pevet P., Gauer F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                        174
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
16116 MW: B6724CE956436A20 CRC64;
                                                                                                                                        19857 MW; 21DDC0437F93BE77 CRC64;
                                                          36.0%; Score 545.5; DB l
59.2%; Pred. No. 5.6e-39;
ative 29; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.5%; Score 582.5; DR 6
81.6%; Fred. No. 3.3e-42;
                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vortebrata; Futeleestomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 AA
                                                                                         DB 11; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 138;
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Best Local 9
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01-FEB-1997 (TrEMBLrel 02, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MEL-1B MELATONIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weaver D.R., Liu C., Reppert S.M. Submitted (MAY-1996) to the EMBL BMBL, U57554; AAB17865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57/BL6;
Weaver D.R., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P70329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VEAICWAPLNCIGLAVAINPEAMALQIPEGLEVTSYFLAYENSCLNAIVYGLLN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 AYTIAVVVEHELVEMIIVIFGYF FIWILVIL VEGEVKPF-PKPKLKPHDFRNEVTMEVVEV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO: IPRO00025: -.
INTERPRO: IPRO000276: -.
PPAM: PF000001: Tum_l: 1.
PRINTS: PR00857: MELATONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 LFAICWAPLNFIGLAVASDPASMVPRIPEWLFVASYYMAYFNSCLNAIISGYWN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Elshourbagy N.A., Ames R.S., Fitzgerald L.F., Foley J.J., Chambers Szekeres P., Schmidt D.B., Buckley P.T., Dytko G.M., Murdock P.R., Tan K.B., Shabon U., Nuthulegantl P., Wang D.Y., Wilson S., Pergsma D.J., Sarau H.M.

"Cloning and characterization of the human HLWAR77, a G-protein coupled receptor.";
                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
G-PROTEIN COUPLED RECEPTOR HIWAR77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QXIMAVVAIHELLEIAVVSFCYLLIKILVISAFEKAKAERKLPLPPSDLPSELIMFAVEV 120
                                                                                                                                                                                                                                                                                                                                    Q9NP49
                                                                                                                                                                                                                                                                                                                 Q9NR49:
                                                                                                                                                                              Eukaryota: Metazoa: Chordata: Cranlata, Vertebrata: 
Mammalla: Eutheria: Primates: Catairhini: Hominidae:
                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AYTIAVVVEHELVEMIIVIECYLRIWILVIQVEQEVKEDEKPKLKEHDERNEVTMEVVEV 183
                                                                                                                        SEQUENCE FROM N A.
                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 L 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 23.5%; Local Similarity 54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 QYIAAVVAIHELLEMAVVSECYLRIWVLVLQAPPKAKATPKLPLPPSDLFSFUTKEAVEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 YCYICHSLKCDKLYSSKNSLCYVLLIWLLT-AAVLPNLPPGTLQYEPRIYSCTFAQSVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YCCICHSTTYHRVCSHWYTPIYISLVWLLTLVALVPNFFVGSLEYDPRIYSCTFIQTAST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AA; 14063 MW, A2376C6E0296CB1C CPC64;
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                                                                                                                                                                                                                                                                                                                                      FRELIMINARY.
                                                                                                                                                                                                   Chordata: Cianiata, Vertebrata; Euteleostomi:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred No. 4.8e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.4
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel 14. Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata; Cianiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primutos; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-PROTEIN-COUPLED PECEPTOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99180505; PubMed=10079187:
MEDLINE-99180505; PubMed=10079187:
Cikos S, Gredor F., Koppel J.;
"Sequence and tissue distribution of a novel G-protein coupled "Sequence and tissue distribution of a novel G-protein coupled "Sequence and tissue distribution of a novel G-protein coupled "Sequence and tissue distribution of a novel G-protein coupled "Sequence and tissue 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y5X5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR000276; -.
INTERPRO; IPR000611; -.
PEAM; PF00001; 7tm_1; 1.
PRINTS; PR00227; GPCPPHODOPSN.
PRINTS; FF01012; NPPEPTIDEYR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 INIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRGFQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 QEQWHVVSRKKQKI-----IKMLLIVALLFILSWLPL--WILMMLSDYADLGFNELQ1 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE - 522 AA; 60300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00237; G_PROTEIN_PECEPTOR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Comm
EMBL; AF119815; AAD22047.1;
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243 VDREQCVVYPER-PKL-TIKTA:VLIMIIWVLAITIMSPSAVXLHVQEEKYYEVELNSUN 300
                                                                                                                                        183 NLFILNLAISULLVGIFCMPITILEDNITAGWFFÖNTMCKISELV<sub>E</sub>ÐISVAASVFTLVAÍA 242
                                                                        62 INRYCYICHSLKCDKLYSSKNSLCYVLLIWLLTAAVLP------NLRRGTLQ 107
                                                                                                                                                                                                            2 NIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTSPVYWCREDWPNQEMRKIYTTVLFANIYLAFLSLIVIMYGRIGISLFPAAVPHTGPKN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INRYCYICHSLKODKLYSSKNSLCYVLLIWLLTAAVLP....----NLRRGTLO 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 AA, 48686 MW, 7A47040EE01FHE67 0FC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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25.4%; Pred. No. 6.9e-16;
                                                                                                                                                                                                                                                                                     18.3%; Score 277.5; DB 4
25.4%; Pred. No. 8.6e-16;
25.4%; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Mismatches 99; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55DE9FD857F77041 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 522;
                                                                                                                                                                                                                                                                                                           Indels 43: Gaps
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A4455852x
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Bukaryora: Mejazoa: Chordata; Cranilata; Vetteleostomi;
Actinoptoryali; Meopteryali; Peleostof; Euteleostof; Estaliophysi;
Typriniformos; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 3
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PRINTS: PR00237. GECREHOESPSN.
PRINTS: PR01012: NPPEPTIDEYE
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EMBL. AF037400: AAC41276.1; -.
ZEIN: ZENC-SENE-986516-797. DETTYA.
INTERPRO: IPRO00276: -.
INTERPRO: IPRO00611; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ringvall M., Berglund M.M., Larhammar D.:
"Multiplicity of neuropeptide Y receptors obening of a third distinct subtype in the zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Arthorner D.)
"Yloning and characterization of a movel neuropeptide Y receptor
subtype in the zebrafish.";
DNA Cell Biol. 16:1457-1363(1997).
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11-AUG-1998 (TrEMBLrel. 07, Last sequence update)
11-AUG-1998 (TrEMBLrel. 14, Last annotation update)
NEUROPEPTIDE Y/FFFTIDE YY FFCEPTOF VA
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| 161 | PDREPKLKPHDFFENFVTMEVVFVLFALCWAPPLETCLAVASDPASMVPRIDEWLTVASYY 220
                                                                    196 IQVCLEVWESQOBKLAYTISLLEEQYCTFLLEMLLIYLBIE-LBEQRBEEBMLEEQISBNS 254
                                                                                                                      112 TYSOUF - AQSVSSAYTIAVVVEHELVEMITVIFOYLFIWILVLQVFQBV-----K 150
                                                                                                                                                                    195 TERHUCIUHI SOWKE ··· SVEUAYIAVLIVWULLACVITSLEELAEHLUISELYSUEPAFUSQ 195
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                                                                                                                                                                                                                 78 SILIANLSVSDILVSVFCLPETVVYTLMDHWIFGALLCRLMPFVQCVSVTVSVLSLVLIA 137
                                                                                                                                                                                                                                                                                                                 2 NIEVVSLAVADUVVAIYEVELVLMSIENNGWNLGYLHOOVSGELMGLSVIGSIENIIGIA 61
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                            17.9%; Score 270.5; DB 13; Length 377; 27.1%; Pred No 2 4e-15; ative 58; Mismatches 113; Indels 25;
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FRINTS, PRODIETY
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PRINTS, 
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01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-JUN-2000 (TrEMBLrel 14, Last annotation updat
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Mol. Pharmacol. 56:396-403(1999).
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Mus musculus (Mouse).
Mus azea, Chordata.
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                                                                       303 PYLYAFLIENDYFIFSEDOIH - ISSILEULNASISCHEBBESTANTVESTHOCHBEL
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                                                                                                                                               230 ATTSCHWNQNEPKEYPPTIVSLYTAPVEFUNSSNOVADBVKWEPSET
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Eutheria: Podentia: Sciuroqnathi: Muridae: Murinae: Mus
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24.8%;
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Fred No. 8.3e-15;
9, Mismatches 129,
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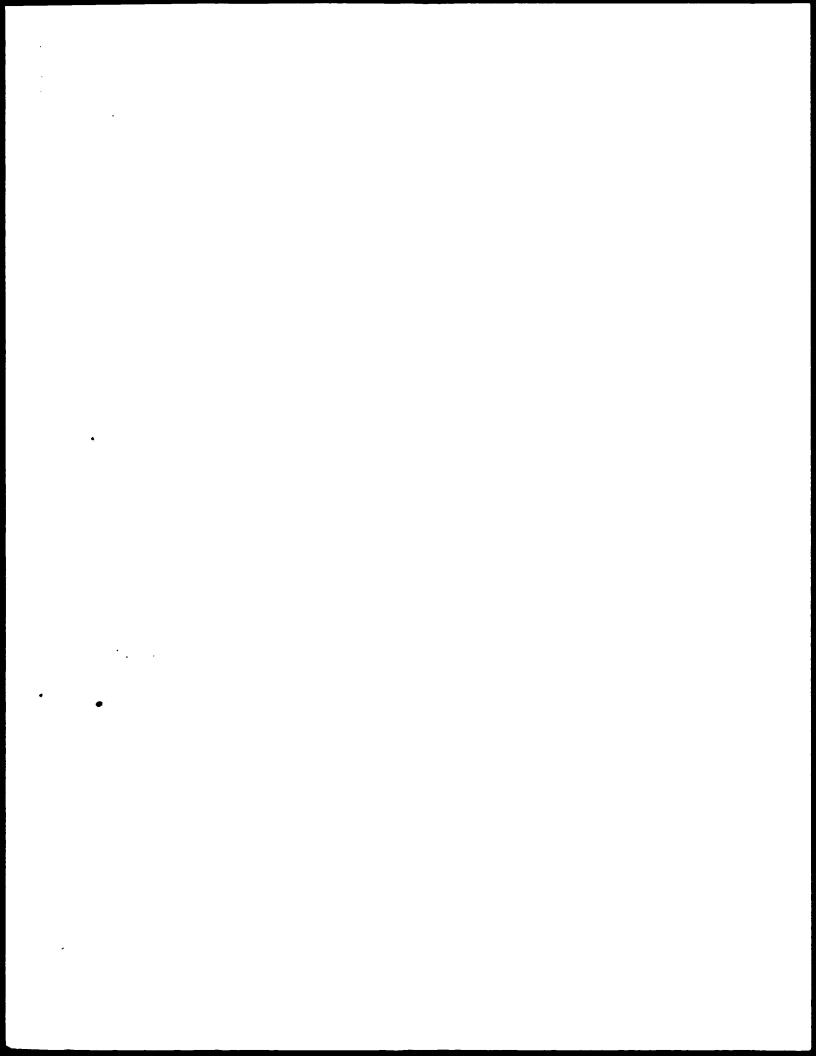
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Eukaryota: Metazoa; Arthropoda; Tracheata: Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota: Diptera: Brachycera; Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
NCSI_TaxID=7227;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
TREHALOSE RECEPTOR 1.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Peppert. S and Ebisawa.T.

DNA encoding high-affinity melatonin receptors

patent: US 5856124-A 11 05-JAN-1999;
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1 (bases 1 to 1050)
Hinuma, K., Kawamata, Y. and Hosoya, M.
PRODUCTION OF PROTEIN OF RECOMBINANT HUMAN MELATONIN RECEPTOR Patent; JP 1997084581-A 1 31-MAR-1997;
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HINUMA KUNIJI, KAWAMATA YUJI, HOSOYA MASAKI
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hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-JUL-1909) to the PORT/EMBL/SenBank databases. Takashi Ebisawa, Saitama Medical Scheol, Lept of Esychiatry: 38 Morohongo, Moroyama-cho, Iruma-gun, Saitama 350-0495, Japan (E-mail-tebisawasatama-mediac.jp, Tel:81-492-76-1213, Fax:81-492-76-1622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ebisawa, I., Kajimura, N., Uchiyama, M., Katoh, M., Sekimoto, M., Watanabe, T., Ozeki, Y., IKoda, M., Jodoi, T., Sugishita, M., Twase, Kamei, Y., Kim, K., Shibui, K., Kudo, Y., Yamada, N., Toyoshima, R., Okawa, M., Takahashi, K. and Yamauchi, T.

Alleic variants of human melaboun has receptor: function and prevalence in subjects with circadian rhythm sleep disorders biochase. Hiophys Post Commun. 42 (3), 832-837 (1999)
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Birren,B., Linton,L., Nusbaum,C. and Lander,E
Home sapiens, close PP11-45013
                                                                                                                      Eukaryota, Metarba; Chordato; Crabiata: Vorrebrata: Piteleostomi;
Mammalia; Eutheria; Primatos; Catarrbibi; Hominidae; Homo.
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Submitted (17-NOV-1999) Whitchead Institute/MIT Center for General Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 26, 2000 this segmence version replaced 91:9183498. http://ftp.genome_washington_edu/RM/RepeatMasker_html All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

Center: Whitehead Institute/ MIT Center for Genome Research

Sequencing vector: M13: M77815; 100% of reads Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.96071 occasensus quality: 137361 bases at least 040 consensus quality: 143060 bases at least 030 consensus quality: 145018 bases at least 020 consensus quality: 145018 bases at least 020 Quality coverage: 4.1 in 020 bases; agarose-fp quality coverage: 4.3 in 020 bases; sum-of-contigs Center clone name: 45_C_13 Insert size: 156000; agarose-fp Insert size: 147217; sum-of-contigs Summary Statistics

* consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is * NOTE: This "is a 'working draft' sequence runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 7160 7259: gap of 100 bp 7250: gap of 1513 bp in length 8783 8882: gap of 100 bp 8783 8882: gap of 100 bp 10395: contig of 1513 bp in length 10396 10495: gap of 100 bp 10727: contig of 1513 bp in length 11728 11827: gap of 100 bp 11828 13650: contig of 1823 bp in length 13751: gap of 100 bp 15262 15361: gap of 1511 bp in length 15262 15361: gap of 1511 bp in length 15362 17846: contig of 1511 bp in length 15362 17846: contig of 1585 bp in length 7159 contig of 7159 bp in length 100 bp of 1523 bp in length 100 bp It currently

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Reppert.S.M. and Ebisawa,T.
DNA encoding high-affinity melatonin receptors
Patent: US 5856124-A 5 05-JAN-1999;
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Neuron 13 (5), 1177-1185 (1994)
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Mammalia; Eutheria, Cetarticdactyla; Ruminantia; Penora; Bovoidea;
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/trasiliftivdivgnltvyrnkkklkrangnvpvpslavadltvavpppplata
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LCyvpriwalvalvynkponkpklkpujpfnevyfvlfatcwaflneigty
VPCYLRIWALVUQVKWXVKPDNKPKLKPUJPFENEVTMEVVFVEXFKITVSLCTTK/
VASDPASMAPRIPEWLEVASYYMAYFNSCLNAITYGLLNQNFRGEYRKTIVSLCTTK/
VASDPASMAPRIPEWLEVASYYMAYFNSCLNAITYGLLNQNFRGEYRKTIVSLCTTK/
                                                                                                                                                                                                               FFVUSSNHVADRIKKRSPLIANHNLIKVDSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pars tuberalis (pituitary)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                              /product="Mel-la melatonin receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAB17721.1"
/db_xref="GI:602132"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="high-affinity receptor"
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                                                                                     70.4%;
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                                                                  Pred. No. 1.4e-129;
0; Mismatches 170;
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                             746 TONGATGGAAGGTGAAACGGGAAACGGAAACTGAAGCCCCAGGACIICAGGAATT
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                                                                                                                                            y Match 70.4%: Score 764: PB 81; Length 1149;
Local Similarity 83.2%; Pred No. 1.4e 129;
hes 885; Conservative 0: Mismatches 170; Indels 9
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                                                                   TACTTCCSATSCTCGTAGTCGTCTTCTCTCTCTCTCAGATCCTCGCCCCTGGTTCTTCTCAGG
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Repperty.S.M. and Ebisawa,T.
DNA encoding high-affinity melatonin receptors
Patent: US 5856124-A 3 05.7NN-1909,
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Submitted (29-7AN-1548) Mol Endocrinol
Rd, Aberdeen AB21 9SB, UK
Location, Cualifiers
1. .1219
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Barrett_P. Conway.S. and Morgan,F.J.
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Fred. No. 2.96-128,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weaver, D.R., Liu, C. and Reppert, S.M.
Nature's Knockent The Mellh melatonin receptor is not necessary
for reproductive an ofreation responses to Sitelian harsters
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On Nov 1, 1996 this sequence version replaced gi.602133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reppert, S.M
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Phharyota: Motaroa: Chordata: Craniata: Vertebrata: Eutaleostomi
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73) Conservative
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GQISASHMGLSVIGSIFNITGIA NPYCYICHSKKUPRVKNGICYVPLIWVLTLV
AIMPNLÖTGTIOQDPRYYSCTFTQSVSSAYTLAVVVEHBIVPNIIVIFCYVLRIWILVL
QVRRPVKPDSKPPLKPQDFPNFVTMFVVFVLFALCWAPLNFIGLLVASDPATMAPPIP
FWLFVASYYMAYFNSCLNAIIYGLLNQNFPQFYKPILVSLFTAKWCFVDSSNDPADKI
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/product="melatorin receptor Mel-la"
/translation="MKCNGSTILLNASGOAPGVGEGGRPRPSWLASTLAFTLIFTTVVD
/translation="MKCNGSTILLNASGOAPGVGEGGRPRPSWLASTLAFTLIFTTVVD
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/dev_stage-"adult"
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Pona A L. Godson, G., Whater, D.B. and Reppert, S.M. Structure, characterization, and expression of the gene enoughing the newser Mella melations receptor Endominology 137 (8), 3469-3477 (1996)
                                                                                                                                                                                                                                                                                                                                              U52222
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                                                                                                         Mammalia: Sutheria: Rodentia: 1 (bases 1 to 1503)

Form, A.L. Codson, C. Woaver!
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Direct Submission
Sieven M. Reppert, Pediatrics,
Submitted (25-MAR-1996) Steven M. Reppert, Pediatrics,
Massachusetts General Hospitul, Fruit Street, Boston, MA 00114, USA
Massachusetts General Hospitul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reppert
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/product='Mel-1a melatonin receptor"
/protein_ig="AAR08755 1"
/db_xref="GI:1326151"
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/strain="BALB/c"
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                                                            ATGTTCTTGTGGAGAGTTCAAATGAAGAAGCAGATAAGATTAAATGTAAGCCCTCTCCA
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 CTCAGGAACTCAGGGAATATATTTGTGGTGAGTTTAGCTGTGGCAGACCTCGTGGTGGC1 24:
                            ctcaggaacgcaggaaacatctttgtggtgagcttagcggtggcagacctggtggtggcc 263
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Reppert, S.M. and Ebisawa, T.

DNA encoding high-affinity melatonin receptors

Patent: US 5856124-A 13 05-JAN-1999;
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Gaueraka, Schusterata, Poirea, Varda, Fevet, R. and Masson Fevet, M. Cloning experiments and developmental expression of both melatonin receptor Mella mRNA and melatonin binding sites in the Syrian
                                                                                                                                                                                       Mesocricetus auratus
Eukaryoth: Motazoa: Chordata: Craniata: Vertebrata: Eutoleosiomi:
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Saisonnières, CNRS-UMR 7518, Universite Louis Pasteur. 12 800
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Mol. Brain Res. (1998) In press 2 (bases 1 to 977) Gauer, F., Schuster, C., Pevet, P. and Masson-Pevet, M.
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/for-tr-in_id="mac67241.1"
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/translation="LNASODABBGGEGSRPRDSWLASTLAFILIFTIVVDILGNULVI
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LSVYRNKKLPNAGNIFVVSLAAADUVVAIYPVPLVLTSIFNNGWNIGYLHCQISAFLM
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/db_xref="taxon:10036"
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Best Local Similarity 83.1%;
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         AP130341 962 bp mRNA Rottus norvegicus melatonin receptor (MT1) mRNA, partial cds AP130341
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Submitted (22-FEB-1999) Laboratoire de Neurobiologie des Fonctions
Rythmiques et Saisonnières, CNRS-UMR 7518, 12 Rue de l'Universito,
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Mammalia; Eutheria;
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Rattus norvegicus
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ILSVYRNKKLRNAGNIFALMNRYCYICHSLKYDRYSNKNSLCYVFLIMTLTLIAIMPNLO
MGLGYIDKRYSCIFICSVSSAYIIALVVFHFVVPMIIVTECVLFIMILVLGVFRFVK
PDSKPKLKPGDFHNEVIMFVVPVLFALGMAPLAFIGLIVASDFAMAPRIPEMLFVAS
PDSKPKLKPGDFHNEVIMFVVPVLFALGMAPLAFTATAVILGGNTANAFRIPEMLFVAS
                                                                                                                                                                                                                                                                                                                                                                                         /qehe="MT1"
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<1 .>982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       /qene="MT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Wistar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism≈"Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata: Euteleostomi: Rodentia; Sciurognathi; Muridae; Mui-nae;
                                                                            score 679.8: DB 11;
pred. No. 3e-114;
0; Mismatches 157,
                                                                               Indels
                                                                                                              Length 982;
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AC012209
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Mammalia; Eutheria; Primates; Catarrhini;
                                  Homo sapiens
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                Motamoa; Chordata: Craniata: Vertebrata: Eutelcostomi;
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454 gcaagaactccctctgctacgtgctcctcatatggctcctgacgctggcgqccgtcctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aagtcagtgggttcctgatgggcctgagcgtcatcggctccatattcaacatcaccygca 393
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                                                                                                                                                                                                                                                                          ATTTCACAAAGGACTACAAAAAAGATTAJCAJTATGCAJAGAJAAGAJGJTCTTTG
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Homo sapiens chromosome 4 clone RF11-390N2 map 4, LON-PASS SEQUENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE. This record contains 323 individual sequencing reads that have not been assembled into sequencing reads that used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generated and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-0071949) Whitehead Institute/MIT Sector for Sectors for Sectors for Sectors for Sectors for Jul 13, 2000 this sequence version replaced qi.0539385.
All repeats were identified using RepeatMasker.
Smit. A.F.A. a Green, F. (1990-1997)
http://fig.ecome.wash.nufen.el/FM/PeppeatMasker.html
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     10.697 10.795; dap of 10.0 bp
10.797 11.599; contid of 794 bp in length
11.591 11.690; dap of 10.0 bp
11.691 12.466; contid of 776 bp in length
                                                                                                                                                 9809 9908: dap of 100 bp
9909 10595: centid of 798 bp
10597 10795: dap of 100 bp
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4485 5295;
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30513 31371 contig of 759 bp in length
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31172 31471; gap of 100 bp
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40305: contin of 764 bp
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44775: contid of 788
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20577: contig of 776 bp
977: gap of 100 bp
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5636; sap of 100 bp
5636; sap of 100 bp
57444; contiq of 808 bp in length
57444; sap of 100 bp
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57544; sap of 100 bp
5833; sap of 100 bp
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45683 45782; gap of 100 bp
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Search completed February 19, 2001, dob-time: 16580 sec

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

Result No.	Socre	Query Query Match Cenyth DR	Congeta	i g		Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists make used to control the initiation or timing of puberty in humans. The receptor dene may also be expressed in a transgenic animal for use as a model system to screen agunists and antagonists.
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This segretor represents the scaling sequence for the house relation receptor protein. This sequence is used in an expression vector designated parks, having the produce the chinese hamster overy (CHO) calls of the invention. The CHO calls express the human melatonin receptor protein, and can be used to identify compounds (such as agonists and antagonists) having affinity to the receptor. The CHO calls can also be used to produce the receptor. The
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or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The

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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                            The sequence encodes a fragment of a human high-affinity melatonin-la receptor, which is a membrane protein, coupled to guanine nucleotide binding proteins (G-proteins). The coding sequence corresponds to the region downstream of the first intron. The gene has been cloned by polymerase chain reaction amplification of human genomic DNA, using primers derived from the Kenpus laevis melatonin receptor sequence (T09947), and use of the product as a probe on a human genome library in phage EMBL-3 under high stringency. The 5'-portion of the gene has been obtained by repushing the DNA library at low stringency, and the complete sequence is given in T09950. Receptor tragments which interact with melatonin, or specific antiboding, may be used is the complete sequence in the sequence of the gene has been obtained by repushing the DNA library at low stringency, and the complete sequence is given in T09950. Receptor tragments which interact with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding high affinity metatonin receptor one - used to identify receptor agenists or antagenists e.g. for regulating circadian rhythm disorders or reproductive cycles
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Conservative

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Score 764: DB 17: Prod No. 3.7e-179; 0; Mismatches 170;

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transcription-polymerase chain reaction amplification of sheep pars tuberalis mpNA, using primers derived from the xonopus laevis melatonin receptor sequence (T09947), and use of the product as a probe on a sheep pars tuberalls cDNA library and a sheep genomic library, to obtain the complete sequence as a hybrid fusion with a 5'-genomic sequence and a 3'-cDNA sequence as a hybrid fusion with a 5'-genomic sequence and a 3'-cDNA sequence as a hybrid fusion with a 5'-genomic sequence and a 3'-cDNA sequence as a hybrid fusion with a 1'-consist sequence as a hybrid fusion of the sequence as a hybrid fusion of the sequence as a hybrid fusion of the action of the sequence as a sequence as a hybrid fusion of the action of the sequence as a sequ
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Sequence like mi.
                                                         animal for use as a model system to screen agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                               which is a membrane protein, coupled to guanine vucleotide is proteins (G-proteins). The gene has been cloned by reverse
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Best Local Similarity
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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                   proteins (G-proteins). The gene has been cloned by reverse transcription spilmerase chair reaction amplification of mouse R2-2 mRNA. The corresponding genomic DNA consists of 2 exons divided by a large (over 8 kb) intron. The 3'-untranslated region is 444 bp long, and includes the polyadenylation signal AUDAAA. A major transcription start site is located about 100 bp upstream of the initiation codon. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Autagonists may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cyrle disorder; ovulation; reproductive cycle; animal breeding; puberty; antibody; transgenic animal; drug screening; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding high affinity melatonin receptor one - used to identify receptor agenists or antagonists -g_{\rm c} for regulating circadian
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Query Match
Best Local Similarity
Matches 867, Conserv
                                                                                                             receptor gene. A claimed needed acid (1) comprises a functional meditorin la receptor gene promoter (II) linked to a reporter gene. Cells containing (I) are used to screen compounds (A) for gene le containing (I) are used to screen compounds (A) for ability to alter transcription from (II) (claimed). (A) that are activators are useful for treating circadian by the disorders in humans (e.g. jet lag, sleep-wake disturbances in the blind or regulation of courties are very large of country) and for control of the reproductive cycle in seasonally breeding animals, while those that are inhibitors are used to control initiation and timing of puberty in humans. Screening for (A) can now be done in cultures of transformed cells which do not naturally express the receptor (which is naturally localised to a few specific sites in the central nervous
                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising melaturin la teceptor promoter and reporter gene oused to transform cells for screening for agents that alter transcription from promoter, e.g. for correcting circadian rhythm disorders or controlling reproduction in animals
                                                                                                                                                                                                                                                                                          This INA sequence comprises the gene coding for mouse melatonin la (Mella) receptor (see W23958). A 466 by fragment of the gene was closed from genemic INA by FFR, and was used to probe a BALB/C adult mouse liver EMBL3 SP6/T7 genomic library to isolate the Mella
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which is a membrane protein, coupled to quantile nucleotide binding competents (G-proteins), and has been cloned by PCR amplification of CD human genomic DNA, using primers based on the 3rd and 6th transmerbrane demains of the Xencrus sequence (T09047), then screening of a human brain cDNA library. The genomic Sequence has CC an intron of about 9.0 kb in the 1st cytoplasmic loop region. CC cll hybrids has been used to localize the human MNTRIB gene to CC chromosome liq1:21. Frimers T0995:5; and frich T0041 have been used to analyse tissue distribution. Property flagments which CC interact with melatonin, or specific antibodies, may be used as 1 creeptor agonists or receptor antagonists. Agonists may be used in theract of disorders, to control ovulation, or in alteration of the productive cycles in seasonally breeding animals. Antagonists may be used as 1 creeptoductive cycles in seasonally breeding animals. Antagonists may be used in 2 receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
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17-JUN-1994;
07-OCT-1994;
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Query Match Best Local Similarity Matches 660, Octobery

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   amino acids shorter than those described in the prior art. This segience is a short form of the nowel computer MEI(TAN 4.5) howen as Mel 1-o(beta). As compared to the short form (T740-K), the difference occurs in the 3 untranslated region (both separate the same protein), which is thought to affect the half-life of the mana. The MEI(TAN 5-separate separate styles) with the separate separate styles are from Xenopus skin kna and amplified using the primers I79367-75. The nucleotide sequence was isolated from modulate receipts as protein which is a 7 transmembrane receipts involved in cellular signalling. MEI(TAN has been shown to modulate interacellular signalling. MEI(TAN has been shown to modulate interacellular source as interacellular states.
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Sequence 1147
                                 intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiastarasa, but uplika MEI (1Ap (T79063) cannot inhibit adenylyl cyclase activity.
                                                                                                                                                                                                                                                                      Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEI-lA. The sequences encode proteins which are 65
                                                                                                                                                                                                                                                                                                                          Claim 1; Page 33-34; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                              cardiovascular disease and cancer
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untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The MEL-lab sequences also differ from known MEL-la receptor sequences by 6 amino acids. The nucleotide sequence was isolated from cNNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-lab has been shown to modulate intracellular CGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike MEL-laa (T79063) cannot inhibit adenylyl
   Sequence 1312 BP; 365 A; 271 C; 267 G; 409
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Rew nucleic acid enoughly functional modatomic receptor of Nemopus Proceeding for potential (ant)agonists useful for e.g. treating Proceding for potential (ant)agonists useful for e.g. treating Proceding for potential (ant)agonists useful for e.g. treating Proceding Sciences and cancer

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XX New nucleic acid enoughly functional modatomic receptor of the Xemopus laevis Control of the sequences of the Xemopus laevis Science acids shorter than the sequences enough proteins which are 65 control of the India and India acids shorter than the sequence is a long form of the novel of the previously known proteins. This sequence is a long form of the novel receptor MEL-laa also known as Mel 1 (alpha). As compared to the short of form (179064), the difference occurs in the 3 unitranslated from Conformation which is thought to affect the sequences enough to sequence was isolated from CON allf-life of the mRNA. The nucleoting which is thought to affect the CONFORMATION of the modes a protein which is a 7 transmembrane of receptor involved in cellular signalling. MEL-laa has been shown to the septiment of the involved in cellular signalling. MEL-laa has been shown to the sequence encodes a protein which is a 7 transmembrane of the sequence of inhibiting its accumulation induced by an inhibitor of the phosphodiesterase.

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17-JUN-1994;
07-021 1994.
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                               DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e^{-\alpha} for regulating circadian
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             The sequences given in 072222.23 are primers which were used to amplify this partial cDNA for the human alpha-IB adrenergic receptor. The sequences given in 072225.26 are primers which were used to amplify the 3' end of the rat alpha-IB adrenergic receptor (see also 072227). The amplified human sequence was ligated to the 3' end of the rat sequence to give the sequence within 10 807879. The complete coding roution for the human/rat alpha-IB adrenergic receptor was subcloned into the eukaryotic expression vector pc0NAI-neo. The resulting plasmid was transfected into COS-7 cells by electroporation. Membranes prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q72224 standard; cDNA; 921 BP.
                                                                                                                                                                                                                                                                        Now that encoding alpha 1C and 1A human adrenergic receptors used to detect selective inhibitors of alpha 1C, useful for treatment of benign prostatic hypertrophy
                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-316922/39
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                                                                                                                                                                                                                                 Example 8; Fig 12; 120pp; English.
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RESULT 15 T11608

Tl1608 standard; cDNA; 921

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(first entry)

Human alpha-1B adrenergic receptor amplified cDNA sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bind to the receptor and alter its function. Truncation at the 3, and of the sequence does not affect the functioning of the receptor, as long as the ligand binding domain and signal transduction segments of the receptor (G-protein interaction) are intact. Cells expressing the 1C receptor are used to identify compounds which bind to this receptor with at least a 12 fold greater affinity than to other adrenergic receptors. Compounds identified this way, are useful for treating the acute symptoms of benign prostatic hypertrophy, particularly when used in conjunction with finasteride. They may also be used to reduce intracular pressure, control arrhythmia and other CNS events related to the 1C receptors, to treat or prevent male pattern baldness, seborihoea, female hirsuitism, prostaticis, prostatic cancer and acne. For treating baldness they may be formulated with a potassium channel opener such as minoxidil. The cloned receptors can be used to screen for tissue specific receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 136; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New saccharin type derivs. - useful as selective alpha 10 adrenergic receptor antagonists for treating e.g. benign prostatic hyperplasia
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Result
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2: (2002_C)Ft.data_C/Int_SE_C/MN.seq *

3: (2002_C)Ft.data_C/Int_SC_C/MMP seq *

4: (2002_S)Ft.data_C/Int_POTUS_COMB seq:*

5: (2002_S)Ft.data_C/Int_Potus_COMB.seq:*
       Match Length DR
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US-08-466-103A-11

; Sequence 11, Application US/08465103A

; Patent No. 5856124

; GENERAL INFORMATION:
US-08-466-103A-11
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ELING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PRILE APPLICATION DATA.
APPLICATION DATA.
APPLICATION MIMBER 08/261,857
FILING DATE: 17-JUN-1994
ATHLENEY/AGENT INCOMMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
COUNTRY: US
CIP 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reppert, Stev APPLICANT: Ebisawa, Taka TITLE OF INVENTION FILE NUMBER OF SELENCES:
                                                                                                          LENGTH: 1085 base pairs
IYPE: nucleic acid
STRANDEDNESS: double
IOPOLOGY: linear
                                                                                                                                                                                                                                   NAME: Fraser, Janis K.
PROISTRATION NUMBER: 34,819
PRIEBENCE/POOKE: NUMBER: 907
TELECOMMUNICATION INFORMATION:
TELECIONE. 617/542-8070
TELEPAX: 617/542-8906
                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows95
SUFTWARE: FastSEU for Windows Version
CURRENT APPLICATION DATA:
                                                                             FEATURE:
              NAME/KEY. Coding Sequence LCCATION: 33...1082
OTHER INFORMATION:
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06-JUN-1995
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OTHER INFORMATION: US-08-466-103A-5
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542-5070
TELEPAX: 617,542-8906
INFORMATION FOR SEL ID NO: 5:
SECTIONEC CHARACTERISTICS
LENGTH: 867 base pairs
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                                                                                                                       Matches 848;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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ATTURNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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APPLICATION NUMBER:
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PPICP APPLICATION DATA:
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CITY: E
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STRANDEDNESS: doub
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STREET: 225 Franklin Street
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Fred. No. 16-190;
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J. Gegueboe R. Application US/08:66103A
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                                                                                                                                                                                                                                                                                                                                                    GENEPAL INFOPMATION: APPLICANT: Reppert, Steven M.
APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: RECEPTORS AND USES THEFEOF
C11.
STATE: MA.
COUNTRY: US
COUNTRY: 02110-2854
"TD: 02110-2854
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                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C STREET: 225 Franklin Street
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TELEFAX: 517/542-8906
INFORMATION FOR SEQ ID NO: 3:
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SEGISTRATION NIMBER: 34,819
PREFERENCE (POCKET NUMBER: 00'
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER 04,20
FILING DATE: 17-UN-1994
ATTIPNEY, A TENT INFOFMATION:
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SOFTWARE: FastSEQ for Windows Version
OPERATION DATA:
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PRIOR APPLICATION DATA:
502 bygoogteetgeecaaceteentypagggabteteeagtacgabeegaagatetactegt 561
                                                          506 AGITGTATAGGGAAGGAATTOOTOTGTGGTAGGTGTTOTGAGGTGAGGGGAGGGGAGGGGG 565
                                                                                                                                                                                                                                                                                                                                                                                                    146 ACGGTGTGGGGGCGGGGCCTGGTGGCTGGCCGCCACCCTGGCATCCTGCATCTTCA 205
                                                                                                                                                                                                                                                                                 266 АĞСТБАЛҚААСҚСАĞĞAАТӘТЕТТЕНӘЎТБАЛҚСТТАҚТАĞ ТАСАĞАЛСТСПТБЕТАС
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OTHER INFORMATION:
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STRANDEDNESS: doub
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83.2%; Fred. No. 3c-176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reppert, Steven M. TITLE OF INVENTION: MELATONIN TITLE OF INVENTION: REGULATOR
                                                 APPLICATION NUMBER: 60/022 185
FILING DATE: 18-JUL-1996
AUTORNEY/ACTIVITY INFORMATION:
                                                                                                                                                                                                          COMPUTER: IRM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PASTED for Windows Version 2 0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
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APPLICATION NUMBER
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NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
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                                                                                                          FILING DATE:
                                                                                                                                                              CLASSIFICATION.
                                                                                                                                                                                FILING DATE
                                                                                                                                                                                             APPLICATION NUMBER:
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Best Tomal Similarity
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INFOFMATION FOR SEC ID NO: 1:
FEATURE
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LENGTH: 2772 base pairs
                                                                      1924 CAGGTCAGACGGAGGGTGAAACCCGACAACAAGACCAAACTTGAAGCCCAAGGACTTCAGG 1983
                                                                                                                                                                                                                                                                                                                                                1684 GACAAAATATACAGTAACAAGAACTOGCTCTGCTACGTGTTCCTGATATGGATGCTGACA 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1444 AAGAAGCICAGGAACICAGRGAATATATTIGTRAGTAGATTTAGCTGTRAGAGACCTCGIG 150
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                                                                                                                                                                                                                                           558 togtgcaccttcgcccagtccgtcagctccgcctacaccatcgccgtggtggtttttccac 617
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LOWARION: 1270 .2328
CTHEP INFORMATION: intron coding sequence between positions 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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TELEFAN __617/542-890
                                                                                     caygtoayacayagygtgaaacotgacogcaaacocaaactgaaaccacaygacttoayg 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                     gtggccatttatccgtacccgttggtgctgatgtcgatatttaaccaacgggtgqaaccctg 3:7
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Pred No 1 4e-168;
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US-08-466-103A-13
                                                                                                                                                              NAME: Fraser, Janis K.
RESISTRATION NUMBER: 34.819
REFERENCE/FONCKET NUMBER: 0078
TELECOMMINICATION (NECHMALISM
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/06446104A Patent No. 5856124
-08-466-103A-13
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APPLICANT: Ebisawa, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: PETERTOPS AND USES THEREOF
NUMBER OF SEQUENCES: 29
COPPESPONDENCE ACCHESS:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/3 FILING DATE: 07-0CT-1994 PRICR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSICATION: 435
CLASSICATION: 435
PRIOF APPLICATION MAIA.
PRIOF APPLICATION NUMBER: 08/319,887
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FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM Windows ??
SOFTWARE: FastSEQ for Windows Version
CUFFENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                          FEATURE:
                                                                                            MOLECULE TYPE:
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            NAME/KEY: Coding Sequence LOCATION: 1...1059
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER FILING DATE: 05-10
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                             CPOLOGY:
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                                          744 gimannalgittgtgggttittginnistttgccatttqctggqctectctgaacttcatt 803
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Patent No. 5856124
                                                                                                                                                                                                                                                                                                                                                    Query Match 44.6%; Score 483.8; DB 2; Length Hest Local Similarity 68.0%; Pred. No. 1.9e-108; Matches 589; Conservative 0; Mismatches 322; Indels
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REGISTRATION NUMBER 34,819
REFERENCE (***YEI NUMBER 30.7*
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX 617/542-3006
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APPLICANT: Reppert, Steven M.
APPLICANT: Fbisawa, Takashi
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APPLICATION NUMBE: 08/26: 857
ETLING DATE: 17-JUN-1994
ACTORNEY/AGENT INFORMATION:
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O'PERATING SYSTEM: Windows95
SUPTWARE: PastSEQ for Windows Version 2.0
O'TRRENT APPLICATION DATA:
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                                   45.6-103A-15
THE PERSONAL CONTROL OF THE CONTROL OF THE PROPERTY OF THE PRO
                                                                                                                    APPLICATION NUMBER: 08/3:
FILING DATE: 07-0CT-1994
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STRANDEDNESS: double
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US-08-466-103A-1
US-08-466-103A-1
S-09-90c-1, Application US/08466103A
Patent No. 5856124
Patent No. 5856124
Patent No. 5856124
PAPPLICANT: PEDEPART, Steven M.
APPLICANT: PEDEPART, TAKASH
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
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Best Local Similarity
Matches 65% Conserv
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REGISTRATION NUMBER: 0.078
REFERENCE/POCKET NUMBER: 0.078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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COMPUTER: IBM Compatible
CORPATING SYSTEM. Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0
CUPPENT APPLICATION DATA.
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Disket
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA
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118 GGGACTCACCTCTGCCCTGGCGGTGGTTCTTATATTCACCATTGTTGGGACGTCCTGGG 177
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                        APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-Yoon
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHAIO ALPHAIO PEOPPENS: 35
NUMBER OF SEQUENCES: 35
LUBRESPONDENCE ADDRESS: 100
                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14 APP-1995
                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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           ATTORNEY/AGENT INFORMATION:
MAME: Appolling, Mary A.
REGISTRATION NUMBER: 34,087
                                                                                                                                   COMPUTER: IBM PC compatible 
'PEPATING SYSTEM: PT-DGS_MS-DGS
SOFTWARE: Patentin Pelease #1 0, Version #1.25
CHERENT APPLICATION DATA:
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REFERENCE/THORET NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24. Application 3. Filmin Patent No. 5760054
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                                                                         APPLICANT: Thompson, Wayne J.
APPLICANT: Huit, Joel R.
APPLICANT: Novemberg, Jennie R.
APPLICANT: Lee, Heer-Yeen
APPLICANT: Ee, Heer-Yeen
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHAIC ADRENEEGIC RECEPTOR ANTAGONISIS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ACCUPES:
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MOLECULE TYPE: CL
HYPOTHETICAL: NO
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3-722 001 17
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SIREET: 126
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TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SED ID NO: 24:
SECTEMET (1867 base pairs
TENGTH: 1567 base pairs
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TELEPHONE: (908)594-3462
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ATTORNEY/AGENT INFORMATION:
NAME: Appelling, Mary A
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PRIOR APPLICATION DATA:
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CPEFATINT SYSTEM: PT-TTS/MS-TTS
SOFTWARE: Patentin Release #1 0, Version #1.25
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US-08-334-698-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 564-0525
TELEX: (212) 422523 CCCP UI
INFORMATION FOR SEQ ID NC: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 49.3%
Matches 266: Consorration
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APPLICANT: Jonath
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CUPRENT APPLICATION DATA:
APPLICATION NUMBER US/08/3/44/5/4
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PRIOR APPLICATION DATA
APPLICATION NUMBER: 1
FILING DATE:
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290 gtogatatttaacaacgggtggaacctgggctatctgcactgccaagtcagtgggttcct 349
                                                     25% 0000ATOTTGT03000T0310TD03000TTCA1001ETTG000AT0GT030GAXCAT 314
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                                                                                                                                                                                                                                                                                                                                                        LOCATION: 124..1683 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: White, John P. PEGISTPATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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STATE: New York
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                               TATCAACCTAACCATGACCGACCTGATCTTAAGATTCACCGTCCTGACCCTTCTCAGCGCC 434
                                                                                                                          ggcgtccgccctagccttcctcatcttcaccatcgtggtggacatcctgggcaacct 169
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DNA Encoding Human Alpha 1 Adrenergic
Receptors and Tses Thereof
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Mismatches 274.
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: OTHER INFORMATION: US-08-228-932-3
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US-08-228-932-3
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APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
APPLICANT: Theresa A Branchok, John M Wetzel and Paul P. Hartiq
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
                                                                                                                                                                                                                                                                            TELEPHONE: (212) 977 9550
TELEPAX: (212) 664 0525
TELEX: (212) 42523 000P UI
INFOPMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SCFTWARE: Patentin Release #1.24
CURPENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                PREFERENCE/POCKET NUMBER 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
PEGISTPATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 10112
COMPUTER READABLE FORM:
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                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                          SEQUENCE CHAPACTERISTICS:
                                                                                    FEATURE:
                                                                                                      ANTI-SENSE:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                      LOCATION:
                                                                                                                                                                   TOPOLOGY:
                                                           NAME/KEY:
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Best Local Similarity
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                                                                              ANTORNEY/AGENT INFOEMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POOKET NUMBER: 411
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATIN: SYSTEM: PC-505/MS-505
SOFTWARE: Patentin Belease #1.24
CURRENT APPLICATION DATA:
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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I: New York
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: (212) 278-04
(212) 391-0526
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VENTION: DNA Encoding Human Alpha 1 Adrenergic
VENTION: Peooptors and Uses Thereof
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US-08-406-855A-3
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Matches 266; Conservation
                                                                                                                                                                                                                                       Sequence 3, Application US/08406855A Patent No. 5861309
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEC ID NO:
                                                                                                            APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Himan
TITLE OF INVENTION: Receptors and Tess
NUMBER OF SEQUENCES: 23
OOBPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECHLE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                COUNTRY:
                                    STATE: New York
                                                         STREET: 1185 A
                                                                            ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
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Pred. No. 7 2e-
O; Mismatches
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Rest Local Similarity 49.38;
Matches 266: Conservative
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LOCATION: 124..1683
OTHER INFORMATION:
C8-405:855A-3
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REGISTRATION NUMBER: 28.678
REFERENCE/COCKET NUMBER: 41337-A-PCT-US/JPW/KDB
RELECOMMUNICATION INFORMATION:
TELEFHONE. (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
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COMPUTER: IBM PC composible
OPERATING SYSTEM PC-1008/MS-1908
SOFTWAPE: Patentin Belease #1.30
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STRANDEDNESS: single
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Pred. No. 7.2e-16: Didels 0
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US-08-722-190-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Gluchowski, Carlos C Forray, George APPLICANT: Chiu, Theresa A Branches, John M Weitzel and Paul E. Hartig Tille of Invention: Use of Alpha-10 Septific Comparations TO THILE OF INVENTION: TREAT SENIGN PROSTATIC HYPERPLASIA NUMBER OF SEQUENCES: 6
COMPRESSIONE APPRESS: 6
COMPRESSIONE ACCUPED & DUNHAM LLP
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SOFTWARE: Patentin Pelease #1 24
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHOX: (212) 391-0525
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READVABLE FORM: MEDIUM TYPE: Floppy
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ANTI-SENSE:
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                                                                                                                                                                          435 POTARAGRIPATIĀRASTARTSAGRĀDICIGĀGĀGSĀKISTISTIRSASAKSTRASSAGROT 494
                                                                                                                                                                                                                                                                                                                                                                                                  110 ggegteegenetageetgegteet varetteanvategtgaf og vafentgggvanet 169
                                                                              150 gatgggcctgagcgtcatcggccccatattoaccatcaccgccatcgccatcgccatcatcccccta 409
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FILING DATE: 4-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE. New York
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1185 Avenue of the Americas
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US-08-244-354-3
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                                              Query Match 9.4%; Score 101.5; DB 3; Length Best Local Similarity 49.3%; Pred. No. 7.2e-16; Matches 266; Conservative 0; Mismatches 274; Indels
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Patent No. 6015819
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION NATA:
APPLICATION NUMBER: MS/08/244,354
FILING DATE: APFIL 1, 1997
CLASSIFICATION: 514
ATTORNEY/AFRIT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFFRENCE/DOWKET NUMBER: 41878-D-PO
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APPLICANT: Charle
                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
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TITLE OF INVENTION: "PSE OF ALPHA-10" SPECIFIC COMPOUNDS FOR TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA NUMBER OF SECTEMEN: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
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                                                                                                                                     LOCATION: 124..1683
OTHER INFORMATION:
244-354-3
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FEATURE:
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STREET: 11
CITY: New
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STRANDEDNESS: single
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                                                                                                                                                                                     NAME/KEY:
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1185 Avenue of the Americas
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                                                                                  Length 1738;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

ACCESSION VERSION KEYWORDS	RESULT 1 CNS05KTS/c LOCUS DEFINITION
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GenBack/LCBS databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetrandon rigroviridis genome. For more information, please take a look at http://www.genoscope.cog/fr/Tetrandon
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Tetracdon nigroviridis
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutoleostomi;
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Bernot.A., Fizames, C., Wineker, F., Brottier, P., Queller, F.
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Submitted (IZ-APP-2000) to the EMPL/SenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracido nigroviridis genome. For more information, please take a look at http://www.genoscope.com/fr/Tetracion
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160024 of library G from Tetraodon nigroviridis, genomic survey
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Bernot,A., Fizames.C., Wilesker,P., Brottler,P., Section,F.
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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constructed from mouse pineal gland. The tag is a string of 5 nucleotides present between the Not I site and the ciligardI track. The library was monstructed as described
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/clone_lib="NIH_BMAP_MPG"
/clone_lib="NIH_BMAP_MPG"
/dev_stage="27-32 days"
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NIH_BMAP_MPG library is a non-normalized library
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Bernot.A. Fizames,C., Wincker,P., Prottier,P., Quetier,F.
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Roost-Crollius H., Jaillon,O., Dasilva,C.,
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/mote="Semoscope sequence in : C083008A302LF1=end : 17"
a 332 c 295 q 179 t 5 others
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                                                                            202 CONCESTACTORESTITATORESCATERIARISTICIBRATIFICIBRATITARISTAGOS 143
                                                                                                                           265 tttatcogtaccogttugtgctgatutcgatatttaacaacgggtggaaacctuggctatc 324
                                                                                                                                                                                                                                                                                     205 tcaggaacgcaggaaacatctttgtqqtgagcttagcggtqqcagacctgqtgqtgqcca
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                                                                                                                                                                               ISCASASCELSASSAASTATTISAINAINAAN ISPANAIPASSESASSISSISTATTAAAN 203
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae:
1 (bases 1 to 440)
NCI-CEAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
This pione is available reyalty
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  a modified polylinker; Sittel: NOT 1; Sittel: Eco R1:
Figual amounts of playmid DNA from three cormalized
libraries (fetal lung NDHL19W, testis NHT, and B-ceil
NCI (GAP GCB1) were mixed, and ss circles were made in
vitro Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was pop-amplified character hybridization reaction and efform the same 3 libraties. The pools of 5,000 clones made
from the same 3 libraties. The pools consisted of
25448-72711, and 7,000s-73109 Subtraction by Monto
consers and M. Fatima Bonaldo. "
80 a 139 c 149 g 72 t
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75 2: DB 93; Length 440; 
Pred No 1 Se-09;
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                                                                                                          y Match
| Local Similarity | 49 1%;
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This clone is available revally-free through LINI, contact the
IMAGE Consortium (info@image lini.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway: Pov 8501, St. Louis, Mc 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Hillier.L. Allen,M. Bowles,L.
Krizman,D. Kucaba,T., Lacy,M.
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                                                                                CONSERVATIVE
                                                                                                                                                                                                                                        5'-GAGAGAGAGACTCGÁGTITITITITITITITITI-3'. The library we size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by In Claudio Schoelder (LNCIE-ALEA Science Park, Trieste, Italy)."
and
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Site_1: Sstl, Ste_2: XhoI: Double-Stranded CDNA was
prepared from human fetal brain tissue 5' and 3'
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Pred. No. 2.7e-09;
                                                                             Mismatches 206
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                                                                                                                                                                                                                                                                                                                      Genescope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1095)
Recent Grollius, H., Jaillon, G., Dasilva, G., Rouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by nenome wide analysis using
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Prest-Crollins, B , Daillon, O
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Tetraodon nigroviridis
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298 a
/kryanism="Tetraodon nigroviridis"
/db_xref="tavon∙99833"
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High quality sequence stop: 353
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@maae.ilni.gov) for further information
Insort Length: 672 Std Error: 0.00
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Okawa, M., Takahashi, K., and Yamauchi, T.,
Genetic polymorphisms of human melatonin lb receptor
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NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contins are impresented as runs %, but the exact sizes of the gaps
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(E-mail:hattori@gsc_rikon_go_jp, NBL:http://19142-778-9923, Fax:BI-42-778-9924)
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Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seed P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y., Fujiyama, Y., Saka, Y
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Contact: hattori@gsd.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 5.66x in Q20 bases: sum-of-contiqs
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                                                                                                                                                                                                                                   79.0%; Score 873; DB 76; Length 160287; 100.0%; Fred. No. 5.6e-136;
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                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1, (bases 1 %) 200596)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo; tapiens chromosome 11, close FF11: 7550
Birren, B., Linton, L., Nusbaum, C., Lander E.,
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COMMENT JOURNAL. TITLE

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Ferreira, FittHoph, W., Forrost, C., Fonke, P., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, T., Lieu, C., Locke, K., Mardonald, P., Marquis, N., Lehoczky, T., Lieu, C., Locke, K., Mardonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McCernan, C., H., Oconnor, T., Octonor, T., Octonor, T., Octonor, T., Octonor, T., Octonor, T., Octonor, T., Charas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Firrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., McCernan, R., McCernan, R., Wu, X., Wheeler, J., Wu, X., Wassiliev, H., Vo, A., Wheeler, J., Wu, X., Wu, X., Wassiliev, H., Vo, A., Wheeler, J., Wu, X., Wu, X., Wheeler, J., Wu, X., Wheeler, J.
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Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Due; 100% of reads
Assembly program: Phrap: version 0.960731
Consensus quality: 198099 bases at least 030
Consensus quality: 194083 bases at least 030
Consensus quality: 194086 bases at least 030
Consensus quality: 194086 bases at least 020
Insert size: 198696; sum-of-contis
Quality coverage: 4.3 in 020 bases; agarose-fp
Ouality coverage: 4.5 in 020 bases; sum-of-contiss
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1277 3998. contid of 2772 bp in length
3994 4098; dap of
4099 6244: contid of 2146 bp in length
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6345 11678; contid of 5334 bp in length
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11779 115551; contid of 4773 bp in length
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Center code: WIBR
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45554 45652: gap of 100 bp
45653 53242: contid of 7590 bp in length
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62867 - 73271, com
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contig of 6349 bp in length
100 bp
10405 bp in length
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/db_xref="taxon:9606"
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Direct Submission
Submitted (01-MAY-1995) Steven M.
Massachusetts General Hospital. 3:
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Childra*, P. and Falm
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/protein_id="AAG17109.1"
/db_xref="G1:10441571"
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                  Direct Submission
Submitted (22-AUG-1994) Steven M. Reppert, Chronobiology,
Submitted (22-AUG-1994) Steven M. Reppert, Chronobiology,
Submitted (22-AUG-1994) Steven M. Reppert, Chronobiology,
Engited No. 1994
Location/Qualifiers
                                                                                                                                                                         Peppert, S.M., Weaver, D.P. and Ebisawa, T. Cloning and characterization of a mammalian melatonin receptor that mediates reproductive and circadian responses Neuron 13 (5), 1177-1185 (1994)
                                                                                                                 Reppert, S.M.
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Mammalia: Eutheria: Primales: Catarrhini; Hominidae; Homo.
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NLLVILSVYRNKKLRNAGNIFVVSLAVADLVVALYPYPLVLMSIFNNGMNLGYLHGOV
SGFLMGLSVYGSIFNTGIAINEVYLGYVEN TYPYPLVLMSIFNNGMNLGYLHGOV
SGFLMGLSVYGSIFNTGIAINEVYLGYLGYLGYULHLITLAAVI
PNLRAGTLOYDPRIYSCTFAQSVSSAYTIAVVVFHELVENIIVLFCYLRIWILVLQVR
OPVKPPRKPKLRPGFRHEVTMFTVFFULFAIGWAPLNFTGIAVASGFAASWPFFFEWL
FVASYYMAYENSCLNAIIYGLLNONFRKEYPPIIVSLCTAFVEFVDSSNDVADRVKWK
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33. .1085
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RS Hinuma: K., Kawamata, Y., and Hosoya, M.

RS Hinuma: K., Kawamata, Y., and Hosoya, M.

PRODUCTION OF PROTEIN OF PROMBINANT HUMAN MELATONIN PROTEIN ALL TO

TAKENA CHEM INC LTD

OS Homo. sapiens (human)

PN JP 1997994581-A/1

PD 31-MAR-1997

PF 26-SEP-1995 IP 1995249177

FI HINUMA KUNIJI, KAWAMATA YUJI, HOSOYA MASAKI

FI HINUMA KUNIJI, KAWAMATA YUJI, HOSOYA MASAKI

FI CLINES: IN AFIR (4)-74 AFIR (4)-74, AFIR (4), AFIR (4)
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Cloning and characterization of a mammalian melatonin receptor that
mediates reproductive and direadian responses
Neuron 13 (5), 1177-1185 (1994)
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Submitted (24-ANR-1944) Steven M
Children's Service, Massachusetts
Boston, MA 02114, USA
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Reppert, S.M., Weaver, D.P. and Ebisawa, T.
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Reppert.S.M. and Ebisawa,T.
INA encoding high-affinity melatonic receptors
Patent: US 5856124-A 3 05-JAN-1999;
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Pred. No. 1.2e-68
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LCYVELIMILIVALIVHLÜVGILJVEDFIIVSCITTGISVSITTGISVSIAVTIAVVVEHFIYDRLV
VVFCYLEIMALVIQVPMKVKFMKVKKLNAGIFFNFVTMFVVFVLFALCMAPLHFIGLV
VASDPDSMAPRIPEMLEVASYYMAYENSCLNAIIVGLLNQNEFGEVPKIIVSLCTKM
VASDPDSMAPRIPEMLEVASYYMAYENSCLNAIIVGLLNQNEFGEVPKIIVSLCTKM
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Reppert.S M. Weaver D F. and Ebisawa.T
Cloning and characterization of a mammalian melatonin
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Submitted (29-AUS-1494) Steven M Fopport, Chirouchiology, Children's Service, Massachusetts General Hospital, 32 Fr Boston, MA 02114, USA
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Weaver, D.R., Liu,C. and Reppert,S M.
Nature's knockout: The Mellb melated in receptor is not necessary
for reproductive an circadian responses in Siberian hamsters
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LIGHLLVILSVERNKKLENAGHLEVVSLAIAGLEVARITETELTSIERNGWHGYLH
COISAFLMGLSVIGSIENITGIAINRYCYLCHSKLKYDRLYSNKNSLCYVFLIWULLVL
AIMPHLGGGTLYCHPTYSCTEFGSVSSAYTAWVWFHFILIPHIIVIFYILPHWILVL
QVRPPVKPDSKPRLKPGDFPNEVTMFVVFVLFAIGWAPLNFIGITVASGPATMAPRIP
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/db_xref="taxon:10044"
/clone="A146"
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/protein_id="AAB17722.1"
/db_xref="GI:1654110"
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/dev_stage="adult"
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Ob 988 GROAGOTOCAACGACGCGGGCGAGCGGGTCAAGAGCAAGCGGTCGCGGCGGCTCATCA 1042

Search completed: February 19, 2001, 00:56:14 Tob time: 16707 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Xenopus melatonin Xenopus melatonin	T79064 T79063	18	1147 1311	34.6	382.4	11 12
	T09949	17	867	34.7	383 8	10
	T79065	18	1312	35.6	393.6	ص.
Xenopus melatonin	T79066	18	1147	35.6	393.6	00
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Melatonin receptor	T60593	18	1050	43.5	480.6	4
High-affinity mela	TOSSSC	17	1085	43 R	483.8	ω
Human melatonin re	X05747	20	1053	43.9	485.4	2
Migh-affinity mel	T09952	17	1105	100.0	1105	μ
Description	ID	DB.	Match Length	Match	Score	NO.
				Query		Result
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ALIGNMENTS

RESULT T09952 Tつ T0

<u>, .</u>

T09952 standard, cDNA; 1105 BP

TU9952;

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07-0CT-1994;
                                                                                                                                                                                                         Melatonin-1b receptor, human, G-protein-coupled receptor; melatonin receptor-agocist, melatonin receptor-antagocist, circadian rhythm disorder, jet-lag; day-night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty; antibody; transgenic animal; drug screening; ds.
                                                                                                              ₩Ç9535320-A1.
                                                                                                                                                                                                                                                                         High-affinity melatonin-lb receptor gene.
                                                                                                                                                                                                                                                                                             16-AUG-1996 (first entry)
        (MASS-) MASSACHUSETTS GEN HOSPITAL
                                                                      07-JUN-1995;
                                                                                            28-DEC-1995.
                                                                                                                                                                                      Homo sapiens
                           95US-0319887
94US-0261857.
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                                                                                                                                   /product= High-affinity melatonin-lb receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which is a membrane protein, coupled to quantize nucleotice binding or proteins (G-proteins), and has been closed by PCR amplification of human genomic DNA, using primers based on the 3rd and 6th transmembrane domains of the Xenopus sequence (T09947), then so repending of a human brain cDNA library. The genomic sequence has an intron of about 9.0 kb in the 1st cytoplasmic loop region. Intron PCR with primers T09953-54 and 43 human-rodent somatic coll hybrids has been used to localize the human MNTPIB gene to chromosome 11q21-22. Primers T09955-56 and probe T09961 have been used to analyse tissue distribution. Receptor fragments which interact with melatonin, or specific antibodies, may be used as interact with melatonin, or specific antibodies, may be used as interact disorders, to control cyulation, or in alteration of chromosomes, to control cyulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
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iilarit; 100.0%; Fred. No. 2.8e-247;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  XO5747 standard; DNA; 1053 BP
(JCRP-) JCR PHARM CO LID
                         19-JUN-1997;
                                                   19-JUN-1998;
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                                                                                                                                                                                                                     Homo sapiens
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                                                   98EP-0111352
                                                                                                                            /transl_except= (pos:745..747, aa:Phe)
/transl_except= (pos:820..822, aa:Phe)
/product= "melatonin*receptor mel-la"
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                                                                                                                                                                                            Location/Qualifiers
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17-JUN-1994;
07-OCT-1994;
                                   Claim 8, Flg 5, 115pp, English
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 The sequence encodes full-length human high-afficity melatorin-la
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melatonin receptor-agonist; melatonin receptor-antagonist; circadia: rhythm disorder; jetting; day-hight cycle disorder; ovulation; reproductive cycle; animal breeding; puberty; antibody; transgenic animal drug screening; ds.
                             ENA encoding high affinity metatonin receptor one - receptor agonists or antagonists e.g. for regulating
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rhythm disorders or reproductive cycles
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Query Match 43.8%;
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Matches 689; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frequency which is a membrane protein, coupled to guanine nucleotide binding proteins (0-proteins). The gene has been cloned by polymerase chain reaction amplification of human genomic DNA, using primers derived from the xenopus laevis melatonin receptor sequence (10947), and use of the product as a probe to obtain clone T09949. Screening of a human hypothalamus cDNA library has resulted in isolation of the full-length clone. Primers T0995-56 amplify a lag to the table of the full-length clone. Primers T0995-56 amplify a language the tissue distribution of this gene for comparison with the molatonin-lb receptor gene (10995). Receptor fragments which interact with melatonin, or specific antibodies, may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor-agonists or receptor antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in homacs. The receptor gene may also be expressed in a transgenic animal for use as a model system to serve agenists and untagonists.
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                                                                                         This sequence represents the coding sequence for the human melatonin receptor protein. This sequence is used in an expression vector beignated parks. MacIFT. The expression control is used to produce the chinese hamster evary (CHO) cells of the invention. The CHO cells express the human melatonic threshold and antagonists and to used to identify compounds (such as agonists and antagonists) having affinity to the melatonic receptor agonists on also be used as an agent for preventing or treating jet lag, sleeplessness, seasonal melanocholia. Altheimer's disease, dementia caused by cerebral thrombosis, various diseases, receptor and this head pressure, caused as an agent for preventing or treating jet lag, sleeplessness, sassonal melanocholia. Altheimer's disease, dementia caused by cerebral thrombosis, various diseases, receptor and also be used as an exclusive regulator. The melatonic investor can also be used as an exclusive regulator. The
                               melationin receptor antagonist can be used as an agent for provent treating melancholia, neurosis, or mental confusion.
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Pred. No. 1.3e-102;
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06-JUN-1994;
17-JUN-1994;
07-OCT-1994;
                                                                                           transcription-polymerase chain reaction amplification of sheep pars ubcralis mPNA, using primers derived from the Yangeus lawyis melatonin receptor sequence (T0094), and use of the product as a probe on a sheep pars tuberalis cDNA library and a sheep genomic library, to obtain the complete sequence as a hybrid fusion with a 5'-genomic sequence and a 3'-cDNA sequence. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-attagonists. Agonists may be used in the thought of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control cyulation, or in alteration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty; antibody; transgenic animal; drug screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T09948 standard;
                                reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                         DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
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                                                                                                                                                                                                                                                             which is a membrane protein, coupled to guanine nucleotide binding proteins (G-proteins). The gene has been cloned by reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reppert SM;
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Sequence
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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mpNA The corresponding genomic DNA consists of 2 exons divided by a large (over 8 kb) intron. The 3'-untranslated region is 444 bp long, and includes the polyadenylation signal AUUAAA. A major transcription start site is located about 100 bp upstream of the initiation codon. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor agonists or receptor-randomists. Agonists may be used in therapy of circadian rhythm discreters such as jet lag or day night cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melatonin receptor agenist: melatonin receptor antagonist; 
mirralian rhythm disorder: jotilag; day-night cycle disorder: 
ovulation; reproductive cycle; animal breeding; puberty; 
antibody; transponic animal; drug screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, to control evulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ನರಿಗಳದಲ್ಲಿ ಸಂಶಿಕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as a model system to screen agenists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transpenic animal for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins (G-proteins).
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N: Mismatches 320;
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promote:
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                                                                                                                                                                                                                      reproductive cycle; jet lag; mouse; ss.
                                                                                                                                                                                                                                                                                                                                  Mouse melatonin la receptur gene
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                                                                                                                    weery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising melatoric la receptor promoter and reporter gene - used to transform cells for screening for agents that alter transcription from promoter, e.g. for correcting circadian rhythm disorders or controlling reproduction in animals
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    of over 13 kb (full sequence not provided)"
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                                        aagcacctggttctaccttggcctgacatggatactaaccataattgccattgtqccaaa
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circadian rhythm disorder; jet-laq; day-night cycle disorder;
cylation, reproductive cycle, animal brooding, puberty.
Claim 7; Fig 4; ll5pp; English
                                             DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian
                                                                                                                                                                                                                                                                                                                                          M-08232454
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High-affinity melatonin-la receptor gene fragment
                                rhythm disorders or reproductive cycles
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                                                                                                                                             Reppert SM;
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07 - OCT - 1994;
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                                                                                                                                                                                                                                                                                                                                                                                                       antibody; transgenic animal; drug screening; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melatonin-la receptor; human; G-protein-coupled receptor
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The gene has been cloned by polymerase chain reaction amplification of human genomic ENA, using primers derived from the Xenopus laevis melatonin receptor sequence (T09947), and use of the product as a probe on a human genome library in phage EMBL-3 under high stringency. The 5'-portion of the gene has been obtained by reprobing the DNA library at low stringency, and the complete sequence is given in T09950. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-antagonists. Agonists may be used as receptor-agonists circadian hythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence encodes a fragment of a human high-affinity melationin-la receptor, which is a membrane protein, coupled to quanthe nucleotide binding proteins (G-proteins). The coding sequence corresponds to the region downstream of the first intron
                                                  as a model system to screen agonists and antagonists.
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Sequence 867 BF, 188 A, 242 C; 212 C, 215 T, 0 other;

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Pred No 3.4e-80;
""ematches 272;
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sequences encode the same protein), which is thought to affect the half-life of the mPNA. The nucleotide sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T79067-75. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-1Aa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular CGMP, esp. inhibiting its accumulation induced by an inhibitor of
                                                                                                                                                                                                                                                                                                                          2 C-terminal amino acids encoded by these sequences are different from the previously known proteins. This sequence is a short form of the novel receptor MEL-lad also known as Mel 1-c(alpha). As compared to the long form (T79063), the difference occurs in the 3' untranslated region (both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences T79063-66 represent novel allelic genes of the Xenopus larvis melatonin receptor MEL-1A. The sequences encode proteins which are 65 amino acids shower than those described in the prior art. Also the lar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1: Page 28:29: £2pp. French.
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                                                                 phosphodiesterase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jockers R.
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Sequence 1147 BF, 317

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242 G: 354 I; 0 other;

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T79063 standard; cDNA to mRNA; 1311 BP

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                                                                                                                                                                                                                                                                                                                               sequences encode the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from cDNA derived from xeopus skin RNA and amplified using the primers T9067-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-laa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular cMMP, esp. inhibiting its accumulation induced by an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        common actors where the model by these sequences are different from the previously known proteins. This sequence is a long form of the novel receptor MEL-lam also known as Mel 1-c(alpha). As compared to the short form (17904), the difference occurs in the 3 untranslated region (both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences T79053-55 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-1A. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. Also the la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding functional melaturin receptor of Xenopus tor screening for potential (ant)agonists useful for e.g. treating
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                                                                               Melatonin receptor; G-protein-coupled receptor; melanophoro; melatonin receptor-ayonist, melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder;
                                                 ovulation; reproductive cycle; animal breeding; puberty; antibody; transpends animal drug screening; ds.
                                                                                                                                                           High-affinity melatonin receptor gene.
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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human melatonin receptor sequences. Perceptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-atagodists. Agonists may be used it therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control cyclation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic business for the receptor gene may also be expressed in a transgenic business for the receptor gene may also be expressed in a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  layvis. The receptor is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins). The cNNA has been cloned from Xenopus dermal melanophores, and expressed in Escherichia coli Flanking DNA sequences of the 1st 2 Met codons both display a Kozak consensus sequence for initiation of translation. The Xenopus sequence has been used for isolation of honologous sheep, mouse and break relations to the content of the consensus sequence.
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Pred. No. 1.9e-79;
9. Mismatches 332; Indels 6.
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sepretable The protein may also be administrated for purposes of amplifying the net effect of a growth hormone secretagogue by providing downstream signalling and diminishing the required dosage of growth hormone secretagogue, or diminishing the effect of an overdosage of a growth hormone secretagogue during therapy. The protein may also be used to screen and identify compounds which bind to it. Such compounds are used in the treatment of conditions which bind to there is a shortage of growth hormone observed in growth hormone deficient children, elderly patients with musculoskeletal impairment and those children, elderly patients with musculoskeletal impairment and those
                                                                                                                                                                                            receptor. The protein, preferably immobilized on a solid support, may be used diagrastically for the determination of the recentration of growth hormone secretagouss, or its metabolities in physiological fluids, e.g. body fluids including serum, and tissue extracts, as for example in patients who are undergoing therapy with a growth hormone in patients who are undergoing therapy with a growth hormone.
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ALIGNMENTS	US-07-928-611-19	US-08-056-051-3	LT-02520-6650-120	US-00-107-011A-17	US-07-928-611-17	US-08-056-051-1	US-08-475-742-3	PCT-US45-04203-3	US-09-206-899-3	US - 08 - 244 - 354 - 3	05-08-722-190-3	US-08-406-855A-3	US-08-468-939-3	US - 08 - 228 - 932 - 3	95 - 08 - 134 - 698 - 3	PCT-US95-04203-1	US-09-206 899 1
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RESULT 1 US-C8-466-103A-15 Sequence 15, Application US/03466103A Patent No. 5856124 GENERAL INFORMATION: US-08-466-103A-15 REFERENCE, DUCKET NUMBER: OU TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-8070 TELEPAX: 617/542-8906 INFORMATION FOR SEQ ID NO: 15: COUNTRY: US ZIF. 02119:3804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compati APPLICATION NUMBER: 08/319.887 FILING DATE: 07-OCT-1994 FRICE AFFLICATION CATA. APPLICATION NUMBER: 08/261.857 FILING DATE: 17-JUN-1994 ATTORNEY/AGENT INFORMATION: CLASSIFICATION: 435 CLASSIFICATION DATA: PRIOR APPLICATION NUMBER: 08/319,887 APPLICANT: Reppert, Steven M. APPLICANT: EDISAWA, TAKASHI TITLE OF INVENTION: HIGH-AFFINITY MELATONIN TITLE OF INVENTION: FELEPIORS AND USES THEREOF NUMBER OF SECTENCES: 29 COSFESS ONDENCE ADDRESS: OPERATING SYSTEM: Windows95 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: MOLECULE TYPE: CDNA FEATURE: SEQUENCE CHARACTERISTICS: CITY: Boston STATE: MA NAME/KEY: Coding Sequence Localion: 13...1098 OTHER INFORMATION: LENGTH: 1105 base pairs TYFE. Lucicic acid STEANLEDNESS, double ADDRESSEE. NAME: Fraser, Janis K REGISTRATION NUMBER: APPLICATION NUMBER: FILING DATE: 06-JUN 5. Eish & Eichardson E.C. 225 Franklin Street IBM Compatible linear Diskette 06-JUN-1995 US/08/466,103A 34,819

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                                                                                                                                                                                                                                                                                                                                                                               NAME: Fraser, Janis K.
PEGISTRATION NUMBER: 34 819
REFERENCE/DOCKEI NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-6006
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1085 base pairs
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PRIOR APPLICATION NUMBER: 08/319,887
APPLICATION NUMBER: 08/319,887
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SOFTWARE: FastSEQ for Windows Version
OTHERENT APPLICATION DATA:
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***OPPRESSONNENCE ANDRESS:
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                                                                                                                                                                                                          NAME/KEY: Coding Settle Control 1082 1082 OTHER INFORMATION:
                                             APPLICATION NUMBER
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STRANDEDNESS: double
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                                               APPLICANT: Reppert, APPLICANT: Ebisawa TITLE OF INVENTION: TITLE OF INVENTION
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/319/887
FILING DATE: 07-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTOPNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEGISTRATION NUMBER: 34,819
PEFERENCE/DOCKET NUMBER: 001
PEFECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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OTHER INFORMATION:
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PEGISTPATION NUMBER:
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ZIF: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617/542-5070 TELEPHONE: 617/542-8906
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TITLE OF INVENTION: MELATONIN IA SECEPTUR GENE
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TURRENT APPLICATION DATA:
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US-08-466-103A-13
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REFERENCE/DOCKET NUMBER: DOTA
TELEPOMMINICATION INCHEMATION
TELEPHONE: 617/542-5070
TELEPAS: 617/542-84%
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
Query Match
Best Local Similarity
Matches 524 Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/41
FILING DATE: 17-JUN-1994
ATTOFNEY/ASENT INFORMATION:
NAME: Fraser Janis K.
REGISTRATION NUMBER: 34.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/319.887 FILING DATE: 07-0CT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS S
SOFTWARE: FastSED for Windows Version
CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 11111 | 1111 | 11111 | 11111 | 11111 | 1111 | 1111 | 1111 | 1111 | 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCLECULE TYPE:
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                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence LOCATION: 1...1059
OTHER INFORMATION:
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RG 18:
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Score 432: EB 2: Length 1062: Pred. No. 1.1e-85; 0: Mismatches 320: Indels
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                                                                                       Sequence 5, Application US/08466103A Patent No. 5856124 GENERAL INFORMATION:
    APPLICANT: Reppert, Steven APPLICANT: Ebisawa, Takashi
                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INPOPMATION
TELEPHONE: 617/542-50070
TELEPAX: 617/542-5005
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/251,857 FILING DATE: 17-JUN-1994 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IRM Compatible
OPERATING SYSTEM: WINDOWS95
SUPTWARE: PastSQ for Windows Version 2.0
TURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SPOURNORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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      195 auchtetttatadaateeetgaagtaegannaanginatintattinntginasintteatinnag 594
                                                                                                      475 fouddeacecected deacatotypertoatestypetestosographagasectsgetases 534
                                                                                                                                                                                                                                                                                                                                                                295 countaatootoutuucoatottotatuanguntyyynontyyyyaygaygaynaotynaag 354
                                                                                                                                                                                                                                                                                                                                                                                                                                             235 quibabtitattottaqtaaatotaqoattaqotqaoniggiggtggnitiniannnian 294
                                                                                   241_AAGAACTGCCTGTGCTACGTGTTCTTTATATTGTTCTTGAC---GGGGGTCTTGCTGCCC_251
                                                                                                                                                                  181 GCCATCAACCGCTACTGIIACAICIGUCACAGICICAAGTGGGACAAACTGTACAGCAGC 249
                                                                                                                                                                                                                                               121 GTCAGTGGGTTGCTGATGGGGGGIGAGGGTGAIGGGGTGGATAITGAAGAIGAGGGGGAIG 180
                                                                                                                                                                                                                                                                85 decadedectitutdatuddectaagegicategaetetgicetteaatateaetgeeate 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 34.7%; Score 383.8; DB 2; Length 867; Local Similarity 67.1%; Pred. No. 3.1e-75; hes 560; Conservative 0; Mismatches 272; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K. REGISTRATION NUMBER: 34, REFERRINGE/IFFTRET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/3 FILING DAIL. 37 JUL-1934
                                                                                                                                                                                                                                                                                                                          61 COSTRUCTOVIDATOTOGATATETAACAACSOSTSSAACSTSSSCTATCISCACTSSSCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence
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22 Franklin Street
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No
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NAME: Fraser, Janis K.
PRAISI RAIION NUMBER: 34,819
REFERENCE/SWOKET HUMBER: 507
TELEPHONE: 617/542-5070
IELEPHONE: 617/542-8906
                                                                                FILING. DATE: 17-JUN-1994
AIT-PNEYMATENT INFORMATION:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
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                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                           APPLICATION NUMBER: 08/319,887 FILING DATE: 07-00T-1994
                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                        COMPUTER: IBM CO
                                                                                                                                                                                                    AFFLICATION NUMBER FILING DATE: OF-H
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                                                                                                                                                                                                                                                                                                                                             STATE:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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COTHER INFORMATION:
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Matches 200
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APPLICANT: ELEKISMA, LEPK J.
APPLICANT: ELIIS, CATHERINE E
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
NUMBER OF SEQUENCES: 5
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INFORMATION FOR SEC 10 NO:
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LENGTH: 1133 base pairs
TYPE: nucleic acid
STPANDEDNESS: single
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SOFTWAFE, FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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COMPUTER PEACABLE FORM:
MEDIUM TYPE: Diskett
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CLASSIFICATION. 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                       Z91 TAICTGCCIGCCGGCCAGCCTGCIGGIGGACAICACTGAGTCCTGGCTGTTCGGCCAIGC
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                                                                                                                                                                                                                                                         284 SANGAZARGINANTAGATARANANTARANANTARANANANTARANGALAKANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANGANTARANG
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Pred. No. 2e-11;
0, Mismatches 161, Indels 3
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                                                                                                                                                                                                                                                                  Querry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5:
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TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: POT/USG
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1133 BASE PAIRS
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ATTORNEY/AGENT INFORMATION:
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WEDTIM TYPE: 3.5 INCH DISKETTE
201 TATOTOCOTOCOGOCAGOGTATTARTARACAICACIGANTECTGGGCTGIICGGCATGC 350
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TITLE OF INVENTION: Human Neuropoptide Receptor NUMBER OF SEQUENCES: 12
                                   285 otaponotaccountaatortoutugeeatettotatgaeggetgggeeetgggggagaga 344
                                                                          231 CACCACACTOACCAACTACTTCATTGTCAACCIGIOOTGGGTGACGTTCIGGTGACTGC 290
                                                                                                                                                  171 COTCOTOGCCCTUGTGGGCAACACGCTGGTCTGCCTGCCGTGTGGGGGAACCACCACAT 230
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                                                                                                                                                                                                                       y Match 8.2%: Score 90.4, DB 4, Length 1133;
Local Similarity 54.9%: Pred. No. 2e-11;
thes 200: Conservative 0; Mismatches 161; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE ZONCKET NUMBER: 36
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OPERATING SYSTEM: MS-DOS
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STRANDEDNESS: SING
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STATE: NEW JERSEY
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                                                                                                                                  Matches 200;
                                                                                                                                            Guery Match 8.2%; Score 90.4; DB 2; Length 1170; Best Local Similarity 54.9%; Pred. No. 2e-11;
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 23,931
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
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LENGTH: 1170 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,
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OPERATING SYSTEM: DOS
SUFIWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,705
FILING DATE: 30-APR-1997
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MEDIUM TYPE: Diskett
                                                   APPLICANT: BERGSMA, DERK J
APPLICANT: ELLIS, CATHERINE E
TITLE OF LIVENTION: NOVEL G-PROTEIN COUPLED
NUMBER OF SEQUENCES: 5
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PRIOR APPLICATION DATA:
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TOPOLOGY:
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TELECOMMUNICATION INFORMATION:
TELEPHONE 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO 1.
SEQUENCE CHARACTERISITIOS
LENGTH: 1209 RASE PAIRS
TYPE: NUCLEIC ACID
STERMANDENNESS: CTIOTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION
NAME: FERRARO, GREGORY D
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MOLECULE TYPE:
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TITLE OF INVENTION: Human Neuropeptide Receptor
NUMBER OF SEQUENCES: 12
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                                               171 CATCATAGOOGTGATAGGCAACACACATAATCTGOOTTAACATGTGAACAAAAAAAAT 236
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                                                                                                                                   y Match 8.2%: Score 90.4: DB 4: Length 1209:
Local Similarity 54.9%: Pred. No. 2e-11:
hos 200: Conservative 0: Mismatches 161: Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08846705 Patent No. 5935814
Cuery Match
Best Local Similarity 54.9%;
Matches 200, Conservative
                                                                                                                                                                                                 IELEX: 846169
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1564 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM
MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ELLIS, CATHERINE E TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: RAINER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                           NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23.
REFERENCE/LOCKET NUMBER:
                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/846,705 FILING DATE: 30-APP-1997
                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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pred. No. 2.1e-11;
0. Mismatches 161
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US-08-846-704-1

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                                                                                                                                                                                                                                       TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows Version 2.0
"TRENT APPLICATION DATA:
APPLICATION NUMBER: US/GR/R46,704
FILLING DATE: 30-APR-1997
CLASSIFICATION: 435
FFIGE APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1564 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION.
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ADDRESSEE: PAINER & PRESTIA
STREET: P O BOX 980
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APPLICANT: ELLIS, CATHERINE E.
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
NUMBER OF SEGUENCES: 4
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 610-407-0700 TELEFAX: 610-407-0701
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                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 23,031
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684 GCCC 687
                                  522 ggcc 525
                                                                    465 ctaccggcg---ctggcacaccccctctgcaratrtgcctcatctggctcctcaccqtqqt 521
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115-08-846-704-3
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: REPGSMA DERK J
APPLICANT: ELLIS CATHERINE E.
TITLE OF INVENTION NOVEL G-PROTEIN COUPLED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURKENT APPLICATION DATA: APPLICATION UNMEER US/08/846,704 FILING DATE: 30-APP-1097
                                                                  REFERENCE/DOCKET NUMBER: GH
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
               TELEFAX: 610-407-0701
TELEX: 846169
                                                                                                    NAME: PRESTIA, PAUL F
PEGISTRATION NUMBER: 23,031
                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                   TELEPHONE:
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PCT-US95-05616-3
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NAME: FERRAPO, GREGORY D.

REGISTRATION NUMBER: 36.134
REFERENCE/DOCKET NUMBER: 3256
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, RYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 RECKEP FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Neuropeptide Receptor NUMBER OF SEQUENCES: 12
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                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT IN
                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05616
FILING DATE: concurrently
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MEDIUM TYPE: 3.5 INCH DISKETTE
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Local Similarity 54.9%:
hes 200; Conservative
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OPERATING SYSTEM:
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STRANDEDNESS: single
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TYPE: NUCLEIC
STRANDEDNESS:
TOPOLOGY: LINE
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531 GCCC 534
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NUCLEIC ACID
DEDNESS: SINGLE
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Swirth completed sebruary 18, 2001, 20-20-34 Job time: 12838 sec

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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID

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12895 Petr 12895 Petr 1289 EJ524 58742 Petr	2400 wd69b 78604 prosp 8500 prosp 87008 1332b 7216 fj33b 7216 fj33b 736849 metr 86689 metr 96689 metr 97702 metr 38702 metr 3885 SALOQU	3917 10284 39897 Tetr 91713 Tetr 56028 Tetr 55676 Terr 79525 6011	75011 Tetra 41230 Tetra 5372 uk31d0 58896 15931 59205 Tetra 0347 au5900	285640	AL284446 Tetra AL341929 Tetra AL341929 Tetra AL3429370 Tetra AL332501 Tetra AL332501 Tetra	Description

ALIGNMENTS

CNSO4CH1			
Silbort	ONSO4CH1	938 bp FNA GSS	21 MAY-2000
DEFINITION	Tetraodon	Tetraodon nigroviridis genome survey sequence T7 end of close	end of clos
	099D15 of	099D15 of library G from Tetrapdom migroviridis, denomic survey	denomic sur
	sequence.		
ACCESSIÓN	AL284446		
VERSION	AL284446.	AL284446.1 GI:8022832	
KEYWORDS	GSS; genor	GSS: denome survey sequence.	

26-MAY-2000

Neoteleostel:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis.
Tetraodon nigroviridis
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Human gene number estimate provided by genome wide analysis using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome. For more information, please t
http://www.genoscope.cns.fr/Tetraodon.
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    856 CCCCCTCATCCCTGAGTGGTTATTCGTGGCTACTTCATGGCCTACTTTAACAGCTG 797
                                               858 tececagatecetgaggggetatttgteactagetaettaettgettattteaacagetg 917
                                                                                                                                                                                                                                                                  798 ctgctgggctccacttaactgcatcggcctcgctgtggccatcaacccccaagaaatggc 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     679 atctgggtgctggtgcttcaggcccgcaggaaagccaagccayagagcaggctgtgcc-t 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                 CIGCIGGGGGGGCTCAATTTCATCGGCCTGGCGTAGCGATCAGATCAAACGTGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                  CACGCCGCATGACGTGAGAAACTTTGTCACCATGTTCGTGGTGTTGTTGCTCTTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302;
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Roest-Crollius, Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Rernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F.,

Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Enteleostomi
Actinopterygii; Neopterygii; Teleostei; Enteleostei; Neoteleoste
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
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This sequence is a single read and was generated as part of a large
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AL341929.1 GI:8235687
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Roest-Crollius,H., Waillon,O., Dasilva,C., Fizames,C., Fisher,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                               Query Match 11.1%;
Best Local Similarity 65.9%;
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                                                                                                                                                             451 ctaccaccudatctaccqqcqctqqcacacccctctqcacatctqcctcatctqqctoct 512
16 CTACAGGGGACIAIACAGGTAGGGGAAGAGTTTGGTGTTTGTTGGGTTAATGTGGGGGAT 75
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Reset-Crollius.H. Jaillon,O. Dasilva,C., Bouneau.L. Fisher,C.,

Rernot.A., Fizames,C. Wincker,P., Brottier,P., Quetler,F.,

Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted (12-APR-2000) to the EMRH,/GenBank/DDBJ databases. This sequence is a simple read and was generated as partial align scale clone-end sequencing project of the Tetracdom nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS04S0S 842 bp DNA GSS 24-MAY-2000
Terrandon higroviridis genome survey sequence T7 end of clone
C07N02 of library H from Terrandon nigroviridis, genomic survey
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Roest-Croilius, H., Jaillon, O., Lasilva, C., Fizames, C., Fisher,
Rouneau, L., Rillault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Motazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Actinoptorydii; Neopterydii; Teleostei; Euteleossei; Neoteleossei: Enzyptorydii: Ctemosquamata: Acanthomorpha: Euacanthomorpha: Holacanthopterydii: Acanthopterydii: Fercomorpha: Tetraedentiformes: Tetraedentudei: Tetraedentidae: Tetraeden.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                        Conservative
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/note-"Senoscope sequence
239 c 164 q 239
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/db_xxef="taxen:39883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   toration/Qualifiers
                                                                                                                                                                                                               Score 122.8; DB 192; Longth 842;
Fred. No. 4.4e-10;
0; Mismatches 92, Indels 72, Saps
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Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
Weissenbach, T
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Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F.
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Submitted (11-CCT-1999) MRC H
Centre, Hinxton, Cambridge, C
blobelp@lpgmp.mrc.ac.uk
Vector: pBluescript II KS
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                                           Z14 AGACGETGCACCIEGIGGEGGCTEC-GICALGACTICATTATATATATATATATATAGCC
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracdom migroviridis
genume. For more information, plasse take a look at
http://www.genoscope.com.gr/Tetracdom.
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Hernot,A., Firames,C., Wincker,P., Brottler,P., Quetler,F.
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Submitted (12-App-2000) to the EMRI/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis scale clone-end sequencing project of the Tetraodon nigroviridis genome For more information, places take a look at http://www.genoscope.chs.fl/Tetraodon.
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Actinopterygii; Neopterygii; Teleostei: Esteleostei: Neosteleostei
Eurypterygii: Ctenosquamata: Acanthomorpha: Esacanthomorpha:
Heladanthopterygii: Acanthopterygii; Fertemorpha:
Tetraodontiformes: Tetraodontoidoi: Tetraodontidae: Tetraodon.
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GSS: genome survey sequence.
Tetraodon nigroviridis.
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Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
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                                                                                                                                                                                                                                                                                      Unpublished
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Best Local Similarity 49.9%;
Matches 201: Conservative
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih gov
                                                                                                                                                                                                                                                                                                                                           Mammalia: Eutheria, Frimates, Catarrhini, Huminidae, Humo
1 (bases 1 to 440)
NCITODAP http://www.ncbi-nlm-nih-gov/ncitogap
National Cancer Institute, Cancer Senome Anatomy Project
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                                                                                              Seq primer: -400P from Gibco High quality sequence stop, 433.
                                                                                                                                             IMAGE Consortium (info@image lini gov) for further information
Possible revorsed clone: polyT not found
                                                                                                                                                                                               Email: Robert_Strausberg@nih gov
This clone is available royalty-free through LLNL : contact
                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Zotgantsm="Tetracodon nigroviridis"

Zotana-senson 99883"

Zotana-senson 99883"

Zotana-lib-"G"

Zotana-lib-"G"

Zotana-senson promiumico ID GORG

Zotta-"GAROSSO 295 g 179 t 5 c
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/Ordanism="Homo sapiecs"
/dk_xr⊷f="taxos 2606"
                                                                      Location/Qualifiers
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Pred. No. 2e-09;
O: Mismatches 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coattascogotactgotacatetgocacageatggood annannyaati 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181;
                                                                                                                                                                                              Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutelmosteni Acetinopterygii: Neopterygii: Teleustel: Eutelmostei: Neopterygii: Ctenosquamata: Acanthomorpha: Phacanthomorpha: Holacanthopterygii: Acanthopterygii: Percomorpha: Tetraodontiformes: Tetraodontoidei: Tetraodontidae: Tetraodon. 1 (bases 1 to 646)
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Tetrapdom migroviridis genome survey sequence PHC-Ori end of clone
093F03 of library G from Tetrapdom migroviridis, genomic survey
2 (bases 1 to 646)
Edest-Crollius, H.,
                                             Unpublished
                                                                        Charaterization and repeat analysis of the compact denome of the freshwater pufferfish Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                               GSS; genome survey sequence.
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                                                                                                                              Weissenbach, J.
                                                                                                                                                      Bouneau, L
                                                                                                                                                                           Poest-Crollius, H
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/clone_lib="Scares_NFL_T_GBC_S1"
/lab_host="pH10B"
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Billault,A., Quetier,F.. Saur
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Salikon, D. . Edeliva, S
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1 do-Ud;
                                                                                                                                                      Saurin, W., Bernot, A. and
                                                                                                                                                                                 Fizames, C
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A1457674 386 bp mBNA EST 13-APF-1999 148606 xl Soares NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2144771 < similar to qb:K76446 ALPHA-1A ASPENEFSIC FECERTOR (HUMAN), mRNA sequence.
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Contact Pohert Strausberg Ph D.
Tel: (301) 406-1550
Email: Robert_Strausberginih.gov
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Pt. 3 No. 1 20-08;
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CDNA Library Preparation: M.B. Soares Lab Clone distribution.
CDNA Library Preparation: M.B. Soares Lab Clone distribution.
Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
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Direct Submission

Submitted (12-APR-2000) to the EMRL/GenRank/DDRJ databases

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetrandon nigroviridis scale clone-end sequencing project of the Tetrandon nigroviridis scale clone-end sequencing project of the Tetrandon nigroviridis
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Hernot,A., Fizames,C., Wincker,P., Rrottier,P., Quetler,F.,
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biohelp@hymp.mrc.ac.uk
Vector: pBluescript II KS
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FESULT 1 R88414

R88414 standard; Protein; 362 AA

16-AUG-1996 (first entry)

R88414,

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Melatonin-1b receptor, human; G-protein-coupled receptor; oyrochrome-c ramily heme binding site; antibody; glycosylation; melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-laq; day-night cycle disorder; ovulation, reproductive cycle, animal breeding, puberty;
                                                                                                                               Modified-site
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                    /note=
102..11
                                                                                                        /note- "N-glycosylation site" 41..65
                                           /note= "Conserved melatonin receptor motif"
77..101
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75 RO
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116..1
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"Transmembrane region-11"
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17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                        site, Receptor framments which interact with molatonin, or specific intibodies, may be used as receptor another, in the second of the second in the respector another site. Associate may be used in the rapy of circadian rhythmedisorders such as jet-lag or day-night cycle disorders, to control involution, or in alternation of reproductive cycles in seasonally broading on minals. Antagonists may be used to control the initiation or timing of puberry in humans. The receptor gene may also be expressed in a transgrapic animal for use as a model system.
                                                                                                                                                                                                                                                                                                                                    transmembrane domain, and an NAXXY motif in transmembrane-7, rather ham NPXXY. A CYICHS motif, which is a consensus site for cytochrome-c tamily beme binding, is present in both 1b and la type temptots. The N-terminus centains 1 consensus N-dlycosylation for the N-terminus centains and new N-terminus centains
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a novel human high-affinity melatonin-lb receptor (moi.wt. 40,188), which is a membrane protein, ecupled quantum nucleotide binding proteins (G-proteins), with 7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thought to affect the half-life of the mRNA. The coding sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signalling. MEL-LAb has been shown to modulate intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike the MEL-lAa protein, it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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/note= "transmembrane domain 7"
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RESULT
R88409
disulfide bond; ligand binding pocket; phosphorylation; cytochrome-c family heme binding site; melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; antibody; animal breeding; puberty; transgenic animal; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melatonin receptor: G-protein-coupled receptor: glycosylation: disulfide bond: ligand binding pocket; phosphorylation;
                               Region
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33..57
/note= "Intracellular domain"
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                                                                                                                                                                     /note= "Residue which may form ligand binding pocket"
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                                                                                                                                                                                                                   "Extracellular loop"
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                  "Conserved melatocin receptor
                                         "Transmembrace region-Vil"
                                                                                                          "Region used to monstruct primer"
                                                                                                                                                   "Intracellular loop"
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                                                                                                                                                                                                                                                                                                                                "Intracellular loop"
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17-JUN-1994;
07-OCT 1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domains IV. V and VI may introduce kinks in the alpha-helices to form of a ligand binding pocket. Phosphorylation sites in the crading may be involved in receptor regulation. Primers from the encoding DNA may be used for isolation of sheep, mouse and human receptor sequences. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-antiqonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to central evulation, or in alteration of reproductive yeles in seasonally breeding animals. Antagonists may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    has an N-linked dlycosylation site typical for G-protein-coupled receptors, and 2 Cys residues in the 1st 2 extracellular loops may form a stabilizing disulfide bond. Pro residues in transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47,424) from Xenopus laevis. The receptor is a membrane protein, coupled to quanine nucleotide binding proteins (G-proteins), and has 7 hydrophobic putative transmembrane domains. The N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a high-affinity melatonin receptor (mol.wt 47,424) from Xenopus laevis. The receptor is a membrane protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding high affinity melatoric receptor one coused to identify receptor agenists or antagonists e.g. for regulating circadian thythmoliantees or reproductive cycles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09535320-A1
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24-JUL-1996;

96WO-FR01167

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor designated MEL-1Aa, also known as Mel 1-c(alpha). The protein differs from previously known receptors by being 65 amino acids shorter and also having 2 different c-terminal amino acids. The protein is encoded by 2 different allels (174363.4) which differ in the 3 encoded by 2 different allels (174363.4) which differ in the 3 encoded by 2 different allels (174363.4) which differ in the 3 encoded region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The coding sequence was isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signalling. MEL-1Aa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular composers allegations of the proteins can modulate intracellular shoes been shown to be the sequence when the sequence were different allegations of the sequence when the sequence were different allegations of the sequence were different and the sequence were different a
                                                         High-affinity melatonin-la receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 25-26; 62pp; French.
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Melatonin-la receptor; human; G-protein-coupled receptor;
                                                                                                                                                                                                                                                         PRR412 standard: Protein:
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06-JUN-1995;
17-JUN-1994;
07-05T-1994;
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melatonin receptor-agonist; melatonin receptor-antagonist;
circadian rhythm disorder; jet-lag; day-night cycle disorder;
ovulation; reproductive cycle; animal breeding; pubcrty;
transgenic animal; drug screening.
                                   DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian
                                                                  N-PSDB; T09950
                                                                                              Reppert SM;
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94US-0319887
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263..2
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147..1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Conserved melaronin receptor motif"
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                                                                                                                                                                                                                                                                                                                "Transmembrane region-VI"
                                                                                                                                                                                                                                                                                                                                     "Intracellular loop"
                                                                                                                                                                                                                                                                                                                                                       "Transmembrane region-V"
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                                                                                                                                                                                                                                                                                                                                                                            "Extracellular loop'
                                                                                                                                                                                                                                                                                                                                                                                                                "Putative cytochrome-c family heme binding site"
                                                                                                                                                                                                                                                                                                                                                                                             "Transmembrane region-IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Intracellular loop"
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Claim 8; Fig 5; 115pp; English

rhythm disorders or reproductive cycles

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Best Local 9
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                                 25 SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melatonin receptor protein; human; chinese hamster ovary cell; CHO cell; jet laq; sleepiessness; seasonal melancholia; Alzheimer's disease; dementia; cerebral thrombosis; high blood pressure; cancer, melancholia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W15786 standard; Protein; 350 AA
                                                                                                                                 25-SEP-1995;
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61.2%; Fred. No. 2.4e+213;
https://doi.org/10.1006/s.com/scheme/
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milarity 61.2%, Fred. No. 2.4e-113;
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Location/Qualifiers
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60.6%;
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Pred. No. 1.4e-112;
3: Mismatches 71;
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RESULT W23958 ID W2

90

W23958 standard: Protein; 353 AA

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Cells containing (I) are used to screen compounds (A) for ability to alter transcription from the promoter (claimed). (A) that are activators are useful for treating circadian rhythm disorders in
                                                                                                                This protein comprises the mouse melatonin la (Mella) receptor, a G-protein coupled receptor that specifically binds melatonin and signals the melatonin-mediated massade of biological events. A
                                                                                                                                                                                                                                                       Nucleic acid comprising melatonin la receptor promoter and reporter gene - used to transform onlis for screening for agents that alter transcription from promoter, e.g. for correction circadian rhythm disorders or controlling reproduction in animals
                                                                   claimed nucleic acid (I) comprises a functional melatonin la receptor gene promoter (see V04644) linked to a reporter gene.
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-120701/11.
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                                                                                                                                                                                                               Disclosure; Fage 32; 46pp; English.
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135..137
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278 .29
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242..266
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10..12
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192..218
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Best Local :
                                                                                    06-JUN-1995;
17 JUN 1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             humans (e.g. )et law, sleep-wake disturbances in the billd or requilation of ovarian cyclicity ) and for control of the reproductive cycle in seasonally breeding animals, while those that are inhibitors are used to control initiation and timing of puberty in humans. Screening for (A) can now be done in cultures of ransformed cells which do not naturally express the receptor (which is naturally localised to a few specific sites in the central nervous
                                                                                                                                                                                                                                                                                                                 melatonin receptor-agonist; melatonin receptor-antagonist; irradian thythm disorder; jet-lan; day-night cycle disorder; ovulation; reproductive cycle; animal breeding; puberty;
                                                                                                                                                                                                                                M19535320-A1
                                                                                                                                                                                                                                                                   Mas mascalus
                                                                                                                                                                                                                                                                                                                                                                       Melatonin-la receptor; mouse; G-protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                          High-attinity melatonin-la receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENA encoding high affinity melatonin to eptor one cosed to identify receptor agenists or antagonists e.g. for regulating circadian thythm disorders or reproductive cycles
Domain
                                                             Ovis aries
                                                                                                melatonin receptor-antawonist; circadian rhythm disorder, jetilaq; day-night cycle disorder, evelation, reproductive cycle, antibody; animal breeding; puberty; transgenic animal; drug screening.
                                                                                                                                                                  Melatonin-la receptor; sheep: G-protrin-roupled receptor-agonist; cytochrome-c family heme binding site; melatonin receptor-agonist;
                                                                                                                                                                                                                                                                                                                                                          PRR4] n etandard Protein.
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                                                                                                                                                                                                                             High-affinity melatonin la receptor.
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Location/Qualifiers 1..43
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06-JUN-1994;
17-JUN-1994;
07-OCT-1994;
                                    The sequence represents a sheep high-affinity melatonin-la receptor, which is a membrane protein, coupled to quantine nucleotide binding proteins (6-proteins), with 7 hydrophobic putative transmembrane domains. Receptor fragments which interact with melatonin, or specific antihodies, may be used as receptor-agonists or receptor-antagonists. Agonists may be used in
     receptor-agonists or receptor-antagonists. Agonists may be used therapy of circadian rhythm disorders such as jet-lag or day-nigh cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                          Claim 6; Fig 2; 115pp; English
                                                                                                                             receptor agonists or antagonists \epsilon \gamma for regulating diredian rhythm disorders or reproductive cycles
                                                                                                                                                 DNA encoding high affinity melatonin receptor one - used to identify
                                                                                                                                                                      N-PSDB: T09948
                                                                                                                                                                                                  Reppert SM;
                                                                                                                                                                                                                     (MASS-) MASSACHUSETTS GEN HOSPITAI
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                                                                                                                                                                                                                                                                                                                                                                                                            sequence is liven in P88412. Receptor fragments which interact with melatoria, or specific antibodies, may be used as receptor-parameters or receptor-antiagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control cycle, or in alteration of reproductive cycles in sassurally breeding animals. Antaonists
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255 VVFVIFAICWAPLNCIGLAVAINPQEMAPQIPEGLFVISYLLAXFNSGLNAIVYGLLNQN 314
                                                                                                                                135 AINRYCYICHSMAYHRIYRRWHTPLHIGLIWLLTVVALLPNEEVGSLEYDPRIYSCTEIQ 194
                                                                                             {\tt 6l~ainrycyichslkedklyssknsleyvlliwllt-aavlpnlrrqtlqyepriys} \textbf{@} {\tt tfaq~119}
                                                                                                                                                                                                  75 GNUFLYSTALATTYVAFYFELLVALEYEGWALGEEHCKASAFYMGUSVIGSVENITAI 124
                                                                                                                                                                l unifvvslavadlvvalypyplvlmsifnsqwnlgylhcqvsqflmglsvigsifnitgi 60
                             sessaytiaeeethflepmiieifoylriwilelqurqrekpdrkpklkphdfrnfetmf 179
                                                                 TASTOYTAAVVVIHELLPIAVVSECYLRIWVLVLQARRKAKPESRLCLKPSELRSFLIME 254
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DB: T09949.
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94US-0319887
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/note= "1
154..176
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213..2
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229..2
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                                                                                                                                                                                                                                                 45.5%. Score 889 5, fP 1
50.5%: Pred. No. 2.9e-91;
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e- "Transmembrane region-V"
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39 VAPALSAVLIVITAVDVVGNLLVILSVLRNRKLRNAGNLFLVSLALADLVVAFYPYPLIL 98

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                                                                                                                                            the lambda EAPII eTNA library was may from meNA of a human female of fetal (17:19 week gestation) brain, using both oilgo (dI) and random-company primers A 500 by PCF product, corresp to part of the coding region (547-1047) of the rat outphan receptor was used to streen the human fetal brain cDNA library as template and a 23-mer forward primer posses 547-569 (25:2340) and a 25-mer reverse primer posses 10:23-10:47 of (05:2341) Six positive plagues where isolated and sequenced. The DNA of companies to the sequences juxtaposed to the library of the DNA closed and its derivs, making it possible to do PCF amplification of a DNA closed in the plasmid's library. The longest clone (hY1-5) of a DNA closed for sequencing analysis 4 specific synthetic primers of the library (25:244) and sequencing only sis 4 specific synthetic primers of the longest primers (25:244 2:2547) and not receive used for manual sequencing of the hyl-5 clones and its define constructs. Thromology processing to study the inhibition of the postractile effort of nonrepartion to study the inhibition of the postractile effort of nonrepartion to study the inhibition of the postractile effort of nonrepartion to the human blood vessels of the postractile effort of nonrepartion to the human blood vessels of costages; and (3) a 3-base mismatched antisons of 190 hY1MM of (05:2330).
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                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 35-36; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding human neuro-peptide Y-peptide YY Y1 receptor - is
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    £35493
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            This sequence represents the human neuropeptide Y (NPY) receptor subtype YI The CDNA encoding this sequence was isolated from human fetal brain and human adult hippocampus cDNA libraries, using the primers given in 240766-67 which correspond to position 672-594 and 48-78 in the rat cDNA clone FCSR, respectively. The longest isolated clone encoded the human NPY receptor subtype YI. This clone was used to probe a human quenchic library which lead to the isolation of the clone kC (see also R35494) which contains the NPY YI receptor gene. The human NPY YI receptor consists of 3 exons and covers approx. 10 kb. The first 57 nuclectides of the 5 untranslated sequence of the human hippocampa! NPY YI receptor mPNA are separated by a 6 kb intron from the second exon. The second intron containing As in figure stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR: domain; primer human; brain; neuropeptide; Y: NPY-Y1; reisolation; clone; fetal; NPY; probe; adult; hippocampus: cDNA subtype Y1; cytoplasmic loop; kC; transmembrane; G protein; ra
                                                                                                                                                                                                                                                                        Disclosure: Page 8-10; 32pp: English
                                                                                                                                                                                                                                                                                                             screening for NPY agonists or antagonists
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23-JUN-1992;
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codon, is located exactly after the fifth transmembrane domain at
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Best Local :
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Disclosure.
                                                                                                                                                                                                                                                                                                                                                 PCR; domain; primer; human; brain; neuropeptide, Y, NPY-Y1, receisolation; clone; fetal; NPY; probe; adult; hippocampus; cDNA lisubtype Y1; cytoplasmic loop; kC; transmembrane; G protein; rat
                                                                                        WPI: 1993-167694,/20
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23-NOV-1991)
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                            Human neuro-peptide Y-Yl receptor and its DNA - useful for screening for NPY agonists or antagonists
                                                                        N-PSDB: 040769
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Pag= 16 18,
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32pp: English
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W09614331-A1
                                                                        Misc-difference 398
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                     Neuropeptide, receptor, NPY, modified, mutant, adenylate cyclase protein, carpied receptor, Bera-adrentic receptor, audist, annagonist, suppressor; inducer; screening; identification; reatment; obesity; diabetes; inxiety; hypertension; condestive heart tailure; cardiac and cerebral vasospasm; condestive heart tailure; cardiac and cerebral vasospasm;
                                                                                                                                                                                                                                                                                                                                                                                           Modified neuropeptide Y receptor (deletion mutant).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WUR014 standard; protein; 398 AA
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                                                                                                                                                                                               Alzheimer's disease; Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1997
                                                                                                                                                                                                                      phrochromocytoma; dandiioneuroblastoma; Huntinddon's disease;
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                                              /note- "Unidentified amino acid."
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333 yyflukufqrd 343
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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1: //ogn__f/prodata.k/iaa/SA_DOMB.pop *
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3: //ogn__f/prodata.k/iaa/SA_DOMB.pop *
4: //ogn__f/prodata.k/iaa/SA_DOMB.pop *
5: //ogn__f/prodata.k/iaa/SA_DOMB.pop *
                                                                                                                        Issued_Patents_AA:*
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Listing first 45 summaries
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GenCore version 4.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                   TELEPHONE 517,542-8000
IBLEFAX: 517,542-8006
INFORMATION FOR SEQUENCE CHARACTERISTICS.
SEQUENCE CHARACTERISTICS.
LENGTH: 352 amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                       FILING DATE 06-JUN-1495
CLASSIFICATION: 435
PHICE APPLICATION DATA:
APPLICATION NUMBER: 08/319.887
FILING DATE: 07-0CT-1994
PRIOR APPLICATION NUMBER: 08/261.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                     NAME: Fraser, Janis K.
PEGISTRATION NUMBER: 34,819
PEBERNOF, OFFICE NUMBER: 1007
PELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: Windows95
SOFTWARE: Fast-SEE for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                MOLECULE TYPE:
FRAGMENT TYPE:
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ATTOPNEY/AGENT INFORMATION:
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ADDRESSEE Fish & Richardson P G.
STREET 225 Franklin Street
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02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 466-103A-2
                                        INTERMATION FOR SEC ID NOT 2.
                                                                                    NAME: Fraser, Janis K.
REGISTATION NUMBER: 34,819
REFERENCE/PWTKEI NUMBER: 000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 517,542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READARLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reppert, APPLICANT: Ebisawa,
                                                                                                                                                                                                    FILING DAIE: 17-JUN-1994
ATTORNEY ATENT INFOSMALLIN
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 "WRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CO
OPERATING SYSTEM-
SOFTWARE: FASTSE
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LENGTH:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/3: FILING DATE: 07-001-1994
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/466,103A FILING DATE: 06-JUN-1995
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                                                                     TELFFAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSENGSFANGGFAGGWAVRPGWSGAGSAKPSRIPKPBWVAPALSAVLIVTIAVDVVGNLL 60
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  420 amino acids
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                                                                617/542-8906
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RECEPTORS AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                        08/319,887
                                                                                                                                                       34,819
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Best Local Similarity 59.4
Matches 215; Conservative
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                                                                                                                         FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PHIGE APPLICATION DATA:
                                                                                                                                                                                    APPLICANT: Reppert, Steven M. APPLICANT: Ebisawa, Takashi
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                     PRIGE APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HIGH-AFFINITY MELATONIN THREEOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 GLSVIGSVENITAIAINEXCYICHSLEYEEKLYNGESTWCYLGUTWIITTTAIVENEEVGS 172
                                                                               APPLICATION NUMBER: 08/319,887 FILING DATE: 07-00T-1994
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                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VILSVI PNPKI PNAGNLELVSLALADLVVAFYPYPLILVAI FYDGWALGEEHCKASAFVM 120
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                                                                                                                                                                                                                                                                                            Diskette
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MOLECULE TYPE: protein FRAGMENT TYPE: internal US-08-466-103A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pothschild, Max F.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Tun-Ping, Yu
IITLE OF INVENTION GENES AND GENETIC MARKERS FOR IMPLITUDE OF INVENTION REPRODUCTIVE TRAITS IN ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Farley, McKee, Thomto, Voorboos & Sease
SIRFET: 801 Grand Avenue, Cuite 2000
                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compartble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Pelease #1 o Version #1 70
CUBPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: PRESER Janis K
REGISTRATION NUMBER: 34,819
REGERENCE, DOCKET NUMBER: 00
TELECOMMUNICATION (NEORMALION:
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                              APPLICATION NUMBER: US/08/806,365 FILING DATE: 18-JUL-1997
                                                                                                                                                                                                                                                                                                                                               CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 GAGSARPSRT-----PRPPWVAPALSAVLIVITAVDVVGNLLVILSVLKNKKLHNAG 75
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREYKRIILAIWNPPHCIQDASKGSHAEGLQSEAF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLFLYSLALADLYVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIA 135
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                                                                                                                                                                                                                                                                               Sequence 2. April: attem TS/09290420 Patent No. 6037131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 20%; Conservative
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Rest Local Similarity
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 515-288-1338 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027.180
FILING DATE: 19-JUL-19-6
AITCHNEY AGENT INFOPMATION:
NAME: Nebel, Heidi S.
PERISTRATION NUMBER: 37.719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
                                                                                                                                 CORRESPONDENCE ADDRESS.
                                                                                                                                                                              APPLICANT: Reppert, Steven M.
TITLE OF INVENTION: MELATONIN
TITLE OF INVENTION: PEGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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LENGTH: 353 amino acid
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                                                                                                                                                               NUMBER OF SECURICES.
                                                                                                                                                                                                                                                                                                                                                                                                                          SOS UNEPKEYENTIVSUITARVEEVESSNEVADEVKWKESE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 ENFPREYKRILLALWNPPHCIQDASKGSHAEGLQSPAP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 MEVVEVLEATCWAFLNETGLAVASDEASMVERTEWLEVASYYMAYENSCINATTYGLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 MEVVEVIEAICWAPLNCIGLAVAINPQEMAPQIPECLEVTSYLLAYENSCLNAIVYGLLN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 AĞSVSSAYTIAVVVEHELVEMIIVIFCYLBIMILVILVBLEVKEDEKERLKEÇLEFENEVI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 TQTASTQYTAAVVVIHFLLETAVVSECYLKIWVLVLQARRKAKPESRLCIKPSTILESETT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 GIAINRYCYICHSLKYDKLYSSKNSLCYVLLIWLITIAAVI FNIFAGTIQYDFRIYSCTF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 AIAINEYOYICHEMAYHRIYEEWHIPLHJOLIWIITVVAIIFNEEVASIEYDERTYSATE 192
                                                                     STPEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE: Melanocyte CELL LINE: human melatonin receptor la
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                        COTINTRY .
                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TE NAGNUEUVSLALAGUVVAEYEYELILVAIEYUMMALMUBHMA AFAEVMHI SVIMSVENIT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY
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                                            STATE:
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02110-2804
                                                                Boston
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                                                                                                                                                                                   MELATONIN 1A RECEPTOR GENE PEGULATORY REGIONS AND USES THEREOF
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MPUTER READABLE FORM

MEDIUM TYPE:

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                                                                                                                                                                                                                                     738-08-466-103A-14
                                                                                                                                                                                     Seppender 14, Application US/08466103A Patent No. 5856124
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                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                            APPLICANT: Roppert, Steven M.
APPLICANT: Ebisawa, Takashi
[CTLE of INVENTION: HIGH-AFFINITY MELATONIN
[CTLE of INVENTION: RECEPTORS AND USES THEREOF
                    NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFOX 617/542-502
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REGISTRATION NUMBER: 34,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 YTTAVVVEHFIVPMIIVIFGYLRIWVLVLQVRRRVKPDNKPKLKPQDFRNFVTMFVVFVL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 CYICHSLKYDKIYSNKNSLCYVFLIWMLILIAIMPNLQIGILQYDPRIYSCTFTQSVSSA 189
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                                                                                                                                                                                                                                                                                                                                   342 RELIVERCIARMSEVESS-NEEADKIKCKPSPLI 342
                                                                                                                                                                                                                                                                                                                                                                                320 KRILLALWNPRHCIQDASKGSHAEGLQSPAPPII 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 FAIGWAPUNGIGLAVAINPQEMAPQIPEGLEVTSYLLAYENSCLNAIVYGLLNQNERREY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 YTAAVVVIHELLPIAVVSECYLRIWVLVLQARPKAKPESPLCLKPSDLRSELTMEVVFVI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 CYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLPNFFVGSLEYDPRIYSCTFIQTASTQ 199
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ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 56.2%; Score 1072.5; DB 3; Length 300, Local Similarity 59.6%; Pred. No. 3.7e-81; Local Similarity 59.6%; Pred. No. 3.7e-81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 18-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 VSLALADLVVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIAINRY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PGGGEGG-----PPPPSWLASTLAFILIFTIVVDILGNLLVILSVYPNKKLPNSGNIFV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/I***KEI NUMBER: 00786/340002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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SYSTFM: Windows95
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US-08-466-103A-4
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                                                             Sequence 4, Application US/08466103A Patent No. 5855124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rest Local :
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GENERAL INFORMATION:
APPLICANT: Peppert,
APPLICANT: Ebisawa,
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM
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CITY: Boston
STATE: MA
                                                                                                                                                                                               RIO KKIIVSIITTAKMEEVESS-NEEADKIKTKESELL 842
                                                                                                                                                                                                                                     320 KRILLALWNFRHCIÓDASKGSHAEGLÓSPAPPII 353
                                                                                                                                                                                                                                                                                   250 FAICWAPLNLIGLIVASDPATMVPRIPEWLEVASYYLAYENSCLNAIIYGHINQNERKEY 309
                                                                                                                                                                                                                                                                                                                         260 FAICWAPLNCIGLAVAINPQEMAPQIPECLEVTSYLLAYFNSCLNAIVYGU NQNERREY 319
                                                                                                                                                                                                                                                                                                                                                                     190 YTIAVVVEHFIVPMIIVIFCYLRIWVLVLQVBBRVKPDNKPKLKPQDFRNFVTMFVVFVL 249
                                                                                                                                                                                                                                                                                                                                                                                                           200 YTAAVVVIHELLPIAVVSECYLPIWVLVLQARPKAKPESRICIKPSDIRSELIMEVVEVI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 OKICHSEKKEKIYSNKNSECKVELIMMEILLIAIMENEOIGIEGKEKKIKSCIEIGSVSSSA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 CYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLPNEFVGSLEYDPRIYSCTFIQTASTO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 VSLAVADLVVAVYEYELVLISILNNGWNLGYLHOQVSAFLMGLSVIGSILNITGIAMNRY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 VSLALADLVVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIAINRY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PGGGEGG-----RPRPSWMASTLAFILIFTIVVDILGNLLVILSVYRNKKLRNSGNIFV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 PGWSGAGSARPSRIPRPPWVAPALSAVLIVITAVDVVGNLLVILSVLENEKLENAGNLEL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 198; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.9%; score 1066.5; DB 2; Length 353; 59.7%; Prod No 1 1e-80; 1ndels 7; itive 58; Mismatches 71; Indels 7;
    Takashi
                      Steven M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/319,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UM .... 957
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US-08-895-365-7
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER 08/28 FILING DATE: 17-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/319.587 FILING DATE: 07-0CT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/28/4---,107A
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                            185 QYDPRIYSCTFTQSVSSAYTIAVVVFHFIVDMIVVVFCYIPIWALVLQVBWKVKDDNKDK 244
                                                                                   305 CLNATIYGILNQNFRQEYRK1:VSICTTKMFFVDSS--NHVADRIKRKPSFLI 355
                                                                                                                                                                        245 LKPQDERNEVTMEVVEVLEAICWAFLNEIGLVVASDPASMAFRIFEWLEVASYYMAYENS
                                                                                                                                                                                                242 LKESDLESETTMETVEFVIEATTWAFFNITGEAVAINFQEMAPQIPEGLEVTSYLLAYENS 301
                                                                                                                                                                                                                                                                                                     182 FYDPRIYSCTFICTASTOYTAAVVVIHFLLPIAVVSECYLRIWVLVLQAREKAKPESELC 241
                                                                                                                                                                                                                                                                                                                                                 125 LSVIGSVESITGIAINPYCCICHSIPYGKLYSGTNSLCYVELIWTLTLVAIVPNLCVGIL 184
                                                                                                                                                                                                                                                                                                                                                                                           122 LSVIGSVENITAIAINRYCYICHSMAYHPIYPRWHTPLHICLIWLLIVVALLENSEVGSL 181
                                                                                                                          302 CLNAIVYGLLNONFKREYKRILLALWNFKHCIQUASKGSH-AEGLOSPAPFII 353
                                                                                                                                                                                                                                                                                                                                                                                                                                       65 VISVYPNKKIPNAGNVEVVSLAVADILVAVYPYPIALASIVNNGWSISSIEGQISGEIMG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ILSVLRNEKLENAGNLELVSLALADLVVAFYPYPLILVAIFYDGWALGEEHCKASAFVMC 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 00
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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ZIF: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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617/542-8906
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pett TYPE: Melanocyte
us-08-895-365-7
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APPLICANT: Rothschild, Max F.

APPLICANT: Tuggle, Chrisopher K.

APPLICANT: Messer, Lori A.

APPLICANT: Tun-Ping, Yu
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TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO:
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NAME: Nebel, Heldi S.
PESTSTEATION NUMBER 37,719
PEPERFENOF/DOOKET NUMBER: 151
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OPERATING SYSTEM: PC-TOOS/MS-DOS
SOFTWARE: PATENTIA Refease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 95/28/896,365
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LENGTH: 366 amino acids
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CORRESPONDENCE ADDRESS:
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                   242 IKPSDLESSITMFVVFVIFAICWAPLNCIGLAVAINDQEMAPQIPEGLFVTSYLLAYFNS 301
                                                                185 [YEFFEIRSCHEIQSVSSAYTIAVVWEREIVEMINVVFCYLEIWALVLQVEMKVKPDNKFK 244
                                                                                                                                                         125 LSVIGSVFSITGIAINPYCCICHSLPYGKLYSGTNSICYVFLTWTLTIVAIVPNTOVGTL 184
                                                                                                           182 EYDPRIYSCIFIQTASIQYTAAVVVIHELLPIAVVSFCYLFIWVLVIQARRKAKPESRIC
                                                                                                                                                                                                  122 LSVIGSVENITAIAINEYGYICHSMAYHEIYEEWHTPLHICL:WELTVVALLPNEFVGSL 181
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CITY: [
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                                                                                                                                                                                                                                                                                               62 ILSVLENRKLENAGNLELVSLALADLVVAFYPYPLILVAIFYFGWALGEEHCKASAFVMG 121
                                                                                                                                                                                                                                                                                                                                          16 NGSSALLNVSQAA------PGAGD----GVRFRPSWLAATLASILIFTIVVDIVGNLLV 64
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801 Grand Avenue, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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N: 435
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58 1*;
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Pred. No. 4e-79;
58; Mismatches 74; Indels 1
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                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: U82251,857
FILIN: DATE: 17-UN-1994
ATTURNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            M-LECULE TYPE: protein FRACMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,88/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617,542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
FITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ropport, APPLICANT: Ebisawa,
255 VVEVIFAR WARENCIGIAVAINEQEMARQIPEGLEVISYLLAYENSCLNAIVYGILNQN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows Version 2 SOFTWAKE: FASTSED for Windows Version 2 WIRRENT APPLICATION DATA:
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                                         120 SVSSAYTIAVVVEHELVPMIIVIECYLEIWILVIQVEQEVKEDEKEKIKEHDEENEVTME 179
                                                                                       195 TASTOYTAAVVVIHELLPIAVVSFOYLRIWVLVLQARRKAKPESRLCLKPSDLRSFLTMF 254
                                                                                                                                                                            145 AINRYCYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLPNFFVGSLEYDFRIYSCTFIQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TORRESPONDENCE ADDRESS
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                                                                                                                                61 AINRYCYICHSIKODKLYSSKNSLGYVILIWILT-AAVLPNIRPGTLQYEPRIYSCTEAQ 119
                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fraser, Janis K. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                   75 GNLFLVSLALAMI VVAFYPYPI II VALFYDGWALGEEHCKASAFVMGLSVIGSVFNITAL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : YOOJOGOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 amino acids
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                                                                                                                                                                                                                                                                                                                                 45.5%; Score 889.5; DB 2; Length 288; 60.5%; Pred. No. 3.5e-66;
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                                                                                                                                                                     Matches 153;
                                                                                                                                                                                        Query Match
best Local Similarity
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ATTUMENTY AGENT INFORMATION:
NAME: Nebel, Heidi S.
NAME: Nebel, Higher: 37,719
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COMPUTER: IBM PC compatible
PEPARIUS SYSTEM: PT-PWS/MS-TWS
SOFTMARE: PATENTIN Pelasse #1 0, Version #1 30
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
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COMPUTER READABLE FORM:
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APPLICANT: Tunile, Chrisopher K.
APPLICANT: Messer, Lori A.
APPLICANT: Tun-Ping, Yu
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ANTI-SENSE:
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                                           154 RWHTPLHICLIWLLTVVALLPNFFVGSLEYDPRIYSCTFIQTASTQYTAAVVVIHFLLPI 213
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61 STNSLCYVELIMMLTLVAIVENLCVGTLQYDERTYSCTETQSVSSAYTIAVVVEHETVEM 120
                                                                                                                                                                                                                                                                                                                    ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                         94 YPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIAINRYCYICHSMAYHRIYR 153
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                                                                                      1 YPLALASIVNDGWSLSSIHCQLSGFLMGLSVTGSVFNITGIAINBYCCTCHSLRYNKLYS 60
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5939264
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                                                                                                                                                                                      43.8%; Score 835; DB 2; Length 257; 59.5%; Fred. No. 9.4e-62;
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                                                                               Matches
                                                                                                  Query Match
Best Local :
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APPLICANT: Rothschild, Max F.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Messer, Lori A.
APPLICANT: Tun-Ping, Yu
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                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 515-288-1338
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0. Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
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                                    139 YOYICHSMAYHPIYPPWHTPLHICLIWLLTVVALLPNFFVGSLEYDPRIYSCTFIQTAST 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Nebel, Heidi S. REGISTRATION NUMBER: 37, PEFFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18 CLASSIFICATION:
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                                                                                                  Local Similarity
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1 YOYICHSLKYDRWYSNRNSLOGVELIOVLILVAIVENLOMGTLGYDERIYSCTTAQSVSS 60
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801 Grand Avenue, Suite 3200
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                                                                             Conservative
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                                                                           s: Score 511; DB 2;
s: Pred No 2.6e-35;
23; Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (317) 276-07
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-POS
SOFTWARE: Patentin Pelease #1 0, Version #1
CUPPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM MEDIUM TYPE: Floppy
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APPLICANT: Cates, Carolyn A.
TITLE OF INVENTION: PHESUS NEUROPEPTINE YI RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                     211 YTTLLVLQYFGPLGFIFIGYFKIYI----PLKPPNNMMDKMPDNKYPSSETKPINIML 265
                                                                                                                                                                                       121 LFAICWAPLNFIGLAVASDPASMAPRIPEWLFV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 QYTAAVVVIHELI:PIAVVSEQYL¤IWVI.VI.QARPKAKPESPI.CLKPSDI.PSELTMEVVEV 258
254 FVVEVIFALDWAPLNCIGLAVAINFLEMARQIFEGLEVISYCLAYENSCONAIVYGOON
                                                                                                    200 YTAAVVVIHELLFIAVVSECYLRIWVLVLQARRKAKFESBLCLKFSDLFSFLT-----M 253
                                                                                                                                                    152 NRHAYVGIAVIWVLAVASSLP-FLIYQVMTDEPFQNVTLDAVKDKYVCFDQFPSDSHRLS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 IFAICWAPLNCIGLAVAINPQEMAPQIPEGLEV 291
                                                                                                                                                                                                                                                                                                                                                         43 LALAYGAVII----LGVSGNLALIIIILKQKEMENVTNILIVNLSFSDLLVAIMCLPFTF 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                      99 VYTLMDHWVFGEAMCKLNPFVQCVSITVSIFSLVLIAVERHQLIINP-----RGWPPN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEFERENCE/DOCKET NUMBER .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/045,186
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                                                                                                                                                                                                                                                                                                         VAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIAINRYCYICHSMAYHPIYRPW--- 155
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Lill Corporate Center
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ARME: ERNSI, MATDAIRS G. REGISTRATION NUMBER: 30,377
REFERENCE/COMMET NUMBER: 187
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APPLICANT: HERZUG, Herbert
APPLICANT: SHINE, John
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COMPUTER: HRM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARF: Patentin Release #1 24
"HRENT APPLICATION DATA
"HRENT APPLICATION DATA
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266 LEIVVAFAVOWLELTIENTVESWNHQIIATONHNLLELLOHLTAMISTOVNETEYGELNK 925
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                                           E54 FVVEVIEAICMARELNOISOLAVAINEDEMARDIERGEEVIEXEELAXENSOENAIVXGEENG SES
                                                                                                                                         800 YRAAVVVTHECODTAVVSECYCRIWVLVLQARBKAKBESRIGLKBKDLBKBCITTTTTTTT
                                                                                                                                                                                         152 NRHAYVGIAVIWVLAVASSLE-FLIYOVMTDEPFONVTLDAYKDKYVGFDGFFSDSHRLS 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                          41 LALAYGAVII----LGVSGNLALIIIILKQKEMRNVTNILIVNLSESDLLVAIMCLPFTF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                   49 VAPALSAVLIVTTAVDVVGNLLVILSVLRNRKLRNAGNLFLVSLALADLVVAFYFYTLIL 98
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                                                                                                                                                                                                                                                                                                                                     99 VAIEYDGWALGEEHOKASAFVMOLSVIGSVENITATAINPYGYTCHSMAYHPIYPPW--- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET
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                                                                                           YTTLLLVLQYEGELGF LEIGYEKIYI - - - - ELKBENNMMOKMRONKYBSSETKEINIML 165
                                                                                                                                                                                                                                          --HTPLHICLIWLLIVVALLPNFFVGSLEYDPRIYSCT-----FlqTAS----Tq 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99;
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555 13th St. N.W., Suite 701-East
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,678
REFERENCE, LOURS I NUMBER: 4474 *-7,71PW/MAT
TELEFONMINIOATION INFORMATION:
TELEFHONE: (212) 278.0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACIERISTICS:
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COMPUTER FRADABLE FORM:
COMPUTER FRADABLE FORDY disk
COMPUTER: IBM PC compatible
OPFFAIING SYSTEM: PC-L-S/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ALIORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUPRENT APPLICATION DATA:
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                                                               [20] KININI VINAMBONIGETETOYEKTYI-----KIKKKUNMMOKMOGNKYRSGETKKINIMI 265
                254 PVVPVIEAICWAPLNCIGLAVAINEQEMAPCIPEGLEVTSYLLAYENSCLNAIVYGLLNQ 313
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                                                                                                                                                     151 NEBAYYGIAVIWVLAVASSLF-ELIYQVMTDFFFQNVTIFAYKDEYVDFDQDSDSDSHPIG 210
                                                                                                                                                                                                 156 --HIPLHICLIWLLIVVALLPNFEVGSLEYDPRIYSCT-----FIQTAS----TO 199
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                                                                                                         POO YIAAVVVIHELLEIAVVSECYLEIWVIVI ÇARREAKEESBI CIKESTIESELI -
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                                                                                                                                                                                                                                                                                     99 VAIFYDHWALDEEHCKASAFVMGLSVIGSVENITATAINFYCYTCHSMAYHRIYKRW--- 155
                                                                                                                                                                                                                                                                                                                                    43 LALAYGAVII----IGVSGNLAHIIIILKOKEMRNVTNILIVNLSESDLLVAIMCLPETF 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: Sin
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Weinshank, Richard L.
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29.2%: Pred. No. 8.4e-21:
Mative 57: Kismatches 117: Indels 42: Gaps
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TYPE: AMINO ACID
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FCT-US93-05039-3
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PCT-US93-05039-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3. Application PC/TUS9305039
GENERAL INFORMATION:
APPLICANT: Claes R. Wahlestedt
TITLE OF INVENTION: Human Neuroper
TITLE OF INVENTION: Receptor of to
TITLE OF INVENTION: Anitsense Olice
TITLE OF INVENTION: Thereto Which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cuery Match 17.8%; Score 340; DB 4; Length 384; Rest Local Similarity 29.2%; Pred. No. 8.4e-21; Matches 89; Conservative 57; Mismatches 117; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (203)268-1951 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
PEGISTRATION UNMBER: 25.824
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: floppy disk
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LENGTH: 384 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOPTWARE: Microsoft word 4.0
CURRENT APPLICATION DATA:
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CITY: Trumbull
STATE: Connecti
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                                          254 FVVFVIFAICWAPLNCIGLAVAINPQEMAPQIPEGLFVTSYLLAYFNSCLNAIVYGLLNQ 313
246 ISIVVAFAVCWLELTIENTVEDWNHQIIATCNHNLLELLCHLIAMISTCVNF1EYGFLNE 225
                                                                                                 211 YTTLLLVLQYEGODJETETCYEKTYT-----BIKRBNNMMDKMBDNKYBSSETKBINIMI 265
                                                                                                                                                200 YTAAVVVIHELLPIAVVSECYLPIWVLVIQAPPKAKPESPLCLKPSDLPSFLT-----M 253
                                                                                                                                                                                                  152 NRHAYVGIAVIWVLAVASSLP-FLIYQVMTDEPFQNVTLDAYKDKYVCEDQEP$DSHRLS 210
                                                                                                                                                                                                                                                 156 --HTPLHICLIWLETVVALLPNFFVGSLEYDPRIYSCT-----FIQTAS----TQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US93/05039 FILING DATE: 19930527 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   99 VYTLMDHWVFGEAMCKLNPFVQCVSITVSIFSLVLIAVERHQLIINP------RGWRPN 151
                                                                                                                                                                                                                                                                                                                                                  99 VAIFYDGWALGEEHCKASAFVMGLSVIGSVENITAIAINRYCYICHSMAYBRIYRRW--- 155
                                                                                                                                                                                                                                                                                                                                                                                                    43 LALAYGAVII----LGVSGNLALIIIILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 VAPALSAVLIVTTAVDVVGNLLVILSVLRNRKLRNAGNLFLVSLALADLVVAFYPYPLIL 98
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Receptor of the Y1-Type and
Anitsense Oligonucleotides
Thereto Which Inhibit Vasoconstriction
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Qy 314 NFRRE 318
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Db 326 NFQRD 330
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Search completed: February 18, 2001, 16:49:55 Job time: 8329 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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PIR_66:*
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1908
1 MSENGSEANGCEAGGWAVRF......EGL<sub>Q</sub>SPAPPIIGV<sub>Q</sub>H<sub>Q</sub>ADAL 362
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Pred No is the number of results gredicted by obtaine to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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beta-40-adrenergio	A55044	428 2	15.7	300	44
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somatostatin recep	R41795	356	15.9	302.5	(A) (X)
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G protein-coupled	152315	370 1	16.0	304.5	36
kappa-type opioid	A44081	440 2	16.0	305.5	رد. ار،
alpha-1B adrenergi	A45121	517 2	16.0	306	34
beta-3-adrenergic	\$32804	400 2	16.0	306	33
glucerost icoid-ind	P40470	, c. t.	در رح سر	10.4	ند! د ۱
galanin receptor 1	I59336	349 2	16.1	307.5	31
alpha-i-adrenerqic	A40491	010 2	16.1	808	30

ALIGNMENTS

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	1 SCLUMINATULIA PARASA SANTAN	301	8 8
	1 OLKERSCHAREN ALEGALFORGEN DER LEVEN SOOR EEN 300 EEU HELDE	241	B 4
	LEYSPRIYSCIFICIASTQYTAAVVVIHELLFIAVVSFCYI PIWVI VI QABPKAKPESBI 	10 (D	3 8
	1 GLSVIGSVENITAIAINPYGYICHSMAVHPIYPPWHTPLHICLIWLLTVVALLPNFFVGS 180	121	F 5
	1 VILSVLENBELENAGNLELVSLALAGILVVAFYFYFFI LVAIFYU-WALVEEH"KASAFVM 120 		7 8
	1 MSENGSKANGGEAGGWAVEFGWSGAGSARFSRIFRFDWVAPALSAVLIVITTAVDVVGNLL 60 	استو مدو	F 9
0;	uery Match 100 0%; Score 1408; DB 2; Length 362; est Local Similarity 100 0%; Pred No 1e-156; atches 362; Conservative 2; Mismatches 0: Indels 0; Gaps	Query Match Best Local Matches 36	Z W iO
	A;Status. preliminary, translated from GB/EMBG/EDBO A;Molecule type: mRNA A;Residues: 1-362 cPES> A;Tross:reformes EMBC/H25341: WID q471103 PIDM AACSO612 1: PID-q471194 C;Superfamily: vertebrate rhodopsin	tatus. olecul esidus ross::	C > A > A > A > A > A > A > A > A > A >
Gusella in huma	Mahle, C.D.: Woaver D.R.: Slaugenhoupt. S.A.: 92, 874-8738, 1995 zetion of a novel melatonin receptor expressed min-a6004613	eppert c. Nat itle: itle: ccessi	¥¥Ö₽üĞ Çüğdek Çüğdek
	Mellb-melatonin receptor - human C/Species: Homo sapiens (man) C/Sate: 31-May laye #serjestestestestestestestestestestestesteste	1b-mel pecies	Mel C;S
		990	I38990

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A:Molecule type: mRNA
A:Residues: 1-289 -NID:
A:Pross-references: EMBL:030509; NID:q1050962; PID:q1050963
A:Pross-references: EMBL:030509; NID:q1050962; PID:q1050963
R:Di:, F:: Yuan: H:: Suramori, K.S.: Hamadanizaden, A.: Lee, F.J.S.: Pang, S.F.: Brown, FERS Lett. 374, 273-278, 1995
A:Price Molecular and tentional characterization of a partial SDNA encoding a normal characterization of a no
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Reppert, S.M. Proc. Natl. Acad. Sci. U.S.A. 91, 6133-6137, 1994
A:Tille: Expression cloning of a high-affinity melatonin receptor from Xenopus dermal mc A:Returence number: 151656; MUID:94286591
A:Accression: 151656
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C:Superfamily: vertebrate rhodopsin
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A:Mollecule type: mRNA
A:Residues: 1-420 <EBL>
A:Cross:references: EMBL:U09561; NID:q505656; PIDN:AAA70185 1; PID:q505667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Reverence number: 872554
A:Accession: 872554
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(bare: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
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C; Superfamily: vertebrate rhodopsin

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A.Title: Coming and characterization of a mammalian melatonin receptor that medicies A.Reference number: 18848; MUID:95033233
A.Recession: 138848; MUID:95033233
A.Recession: 13884; Francisch from PR.EMEL.TORJ
A.Starus [Fellmining] Francisch from PR.EMEL.TORJ
A.Molecule type: mRNA
A.Residues: 1-340 kKRS
A.Cross-references: EMBL.014108; NID:q602129; FIDN:AAB17720.1: FID:q602179
C:Superfamily: Vertabrate rhedopsin
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C.Date: 29-May:1998 #sequence_remision 29 May:1999 #text_chango in-Apr-inn)
C.Accession: I38848
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で:Species: Номо sapieus (man)
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                                                                                                                         243 VEVLEATOWAPLNEIGLAVASDPASMVERIPEWLEVASYYMAYENSOLNATTYGLLNONE
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                                                                                                                                                                                                                                                                                                                                                                                            123 INPYCYTCHSLKYDKLYSSKNSLCYVLLIWLLTLAAVLPNLFAGTLQYDPRIYSCTFAQS 182
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REPRETIVE CTARVEFUDS SNDVADRVKWKPSP
                                                          415 REEYKEILLALWNERHOIDDASKOSHAEGLOSEAE 350
                                                                                                                                                                                                                                                            153 VSSAYTIAVVVEHFLVEMIIVIFGYLFIWTIVIGVEGEVKEURKEKLKEGDEENEVIMEV 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 205; Conserv
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                                                                                                                                                                                          VEVIEATUMAELNOIGLAVAINFQEMARQIFEGLEVISYLLAYENSCLNAIVYGLLNQNF 815
                                                                                                                                                                                                                                                                                                                       ASTOXIAAVVVIHELLPIAVVSECYLEIWVLVLQAERKAKFESELCLKFSDLRSFLIMEV 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           INEYCYICHSMAYHEIYFEWHTELHICLIWLLTVVALLENFEVGSLEYDPRIYSCTEIQT 195
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F:Reppert, S.M.; Weaver, D.R.; Ebisawa, T.; Mahle, C.D.; Kolakowski Jr., L.F. FRBS Lett. 386, 219-224, 1996
A:Title: Cloning of a medatonin-related receptor from human pituitary.
A:Peference number: $70520 MJID-96228068
A:Accession: $70520
                                                                                                                                                                                                                                                                                              A:Status: preliminary, nucleic acid sequence not shown A:Moleoule type: mPNA A:Residues: 1-613 <PEP>
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A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates re A:Reference number: I38848: MIID:05033233
A:Accession: I46469
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C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Dec-199* *sequence_revision 19-Dec-1997 *text_change 17-Mar-2006
C:Accession: I46469
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respecies Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S70520
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C:Superfamily: vertebrate rhodopsin
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A: Residues: 1:366 < REP:
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                                                                                                                         Matches 151.
                                                                                                                                                                                                                                                                  Best Local Similarity Matches 205; Conserv
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(3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 LSVIGSVESITGIAINRYCCICHSLRYGKLYSGTNSLCYVFLIWTLTLVAIVENLCVGTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 LSVIGSVFNITAIAINRYCYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLFNFFVGSL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 VESVYPNKKERNAGNVEVVSLAVADLEVAVYPYPLALASIVNNGWSESSEHOOLSGELMG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ILSVLPNPKLPNAGNLFIVSLALADIVVAFYPYPLILVAIFYDGWALGEEHGKASAFVMG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 NGSSALLNVSQAA------PGAGD---GVPPPPSWLAATLASILIFTIVVDIVGNLLV 64
17 KLPQPEY-PPALIIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNIFVVSLSVADM 75
                                                        P2 STEPPEWWAPAL . . . SAVLIVTTAVEVVCNLLVILSVLFNPKLFNACNLFLVSLALADI. 87
                                                                                                                                                  Local Similarity
                                                                                                                                                                                 Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKPSDLRSFLTMFVVFVTFATGWAELNGIGLAVAINEGEMAPGIPEGLEVISYLLAYENS BÛL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYDPFIYSOTFIQTASTQYTAAVVVIHELLETAVVSFTYLBIWVLVLQA65KAKPESKL1 141
                                                                                                                      Conservative
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                                                                                                                      44 8%: Scorp 854 5; DR 2; 49.7%; Pred. No 7.10-66; attivo 76 Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.9%; Score 1048; DB 2; Length 366; 58.1%; Pred. No. 9.6e-83; rative 58; Mismatches 74; Indels 1
                                                                                                                   Mismathber 66, Indels 11,
                                                                                                                                                                              Length 61%;
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A. Status, preliminary, translated fo
A.Molecule type: mRNA
A. Fessiones 1976: APESS
A. Cross references EMBL 0114469, NII
C. Superfamily: vertebrate rhodopsin
                                                                                                                                                                                         melaturin receptor - rat (fragment)
C:Species: Ratius norvegizous (Norway rat)
C:Date: 02-Aug-1906 #sequence_revision 02-Aug-1906 #text_change 20-Apr-2000
C:Accession: 162107
S:Feppert, S.M.; Waaver, D.R.; Fhisawa, T.
Neuron 13, 117-1185, 1994
A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates
A:Poforcesion: 162107
A:Accession: 162107
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A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates A;Reference number: 138848; MUID:95033233
A;Accession: 184498
A;Status. preliminary, translated from GE/EMEL/EDBJ
A;Status. preliminary, translated from GE/EMEL/EDBJ
A;Molecule type: mRNA
A;Residues: 1-156 (ARES-A):10-385-references. EMBL/U14110. NIL-3502133. Fiz.;502134
C:Superfamily: vertebrate rhodopsin
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R;Reppert, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melatonin receptor - striped hairy-footed hamster (fragment)
C;Species: Phodopus sungorus (striped hairy-footed hamster)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Apr-2000
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Best Local Similarity
Matches 97, Jonsey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FAICWAPLNFIGLIVASDPATMAPRIPEWLFVASY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 FAICWAPLNCIGLAVAINPOEMAPOIPEGLEVTSY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 YTAAVVVIHELLPIAVVSFCYLPIWVIVIQAPRKAKPESPICIKPSDIRSFLIMEVVEVI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 CYICHSMAYHKIYKKWH1PLHICLIWLLTVVALLPNEFVGSLEYDPPIYSCIF1QTASIQ 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TABAAAMIABAGGGASTBAASGGAAABBAAGTATIMIETATATATATATATAHBAAAAVILIA [5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 VVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIAINRYCYICHSMA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CYTCHSTKYDPTYSNKNSDDYVFLTIWVLTTVATMPNIQTGTTTQYDPKTYSCTFTQSVSSSA 60
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                                                                                                                                                         preliminary, translated from 38, EMSE, TIBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFLLPIAVVSFCYLRIWVLVLQARRKA--KPESRLCLKPSDLRSFLTMFVVFV1FAICWA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YERIFSVRNTÇIYLVITWIMTVLAVLPNMYIGTIEYDPRTYTÇIENYLNNPVFTVTIVÇI 195
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                                                   EMBL 014469, NIO 9652135, PION:AAA57191.1; PIO:g852136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31, Indels
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A:Note: sequence extracted from NCHI backbone (NCHIP:108538)
R:Laribammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlested, C.
J. Biol. Chem. 267, 10935-10938, 1992
J. Biol. Chem. 267, 10935-10938, 1992
A:Tille: Chem. 267, 10945-10938, 1992
A:Tille: Chem. 267, 10945-10938, 1992
A:Tille: Chem. 267, 10945-10938, 1992
A:Returence number: A42773, MUID:92283792
A:Accession: A42773
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A.Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBIP:128000)
Robertour, H.L. Hort, Y.C., Rall, H.J., Bayes, G., Shine, J., Selkie, C.A.
Proc. Natl. Acad. Sci. G.S.A. 89, 5794-5798, 1992
A.Title: Closed human neuropoptide Y reseptor couples to two different second messenger
A.Roteronce comber. A45133. MUID.92335184
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A. Biol. Chem. 268, 6703-6707, 1993
A:Title: Genevaic organization, Localization, and allelic differences in the gene for the A:Reference number: A45490: MUID:93203272
                                                                                                          E:118-136/Domain: transmembrane #status predicted <TM3> E:155-179/Domain: transmembrane #status predicted <TM4> E:260-232/Jownain: transmembrane #status predicted <TM5> E:261-236/Jownain: transmembrane #status predicted <TM5> E:261-236/Jownain: transmembrane #status predicted <TM7> E:261-236/Jownain: transmembrane #status predicted <TM7>
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A:Experimental source: Tetal brain
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Filth, finding site: parbohydrate (Asn) (covalent) *status predicted Filth/Rinding site: palmitate (Cys) (covalent) *status predicted
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Best Local s
Matches 95
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Poywords, appetites 3 protein-coupled receptor; glycoprotein; lipoprotein; thiolester
(3) 66/formus transmembrane Estatus predicted IMIN
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                                                                                 11 198/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 CYTCHSMAYHPIYPRWHTPLHICLIWLLTVVALLPNFFVGSLEYDPPIYSCTFIQTASTQ 199
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nes 95; Conservative 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 KHE27
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Oursey Match

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Score 340;

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A.Gress-references GDB 119604 OMIN 182450
A.Map position: 3q28-3q28
C:Superfamily: vertebrate rhodopsin
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A; Residues: 1:363 <RI
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[[tuto | t] | Tulo 1400 | #species | Two 1400 | #species | 1400 | 1400 | 1400 | 157955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Status. preliminary, translated from GR/EMBI/IDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 107; Conserv
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                            231 ------REKAKPESELCIKPSDLRSFLTMFVVFVIFAICWAP---LNCIGLAVAINPQEM 281
234 PVGCVBBSEEKVTEMVI----
                                                                                                                                                                                                                                    126 SVECTTVMSVDPYLAVVHPLS----SARWRPPPVAKLASAAAWVLSLCMSLPLLVFADVO 181
                                                                                                                192 BBSTCNASWEEFVGLWGAVEI----IYTA---VIGEFAPLLVIGLGYILIVVFVPAAGV 233
                                                                                                                                                                      127 SVENITATATNEYCYTCHSMAYHRIYERWHTP----LHICLIWLLTVVALLENEFVGSLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REE URORD RED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 NRHAYYGIAVIWVLAVASSLP-FLIYQVMTDEPFQNVILDAYKDKYVCFDQFPSDSHRLS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 --HIPLHICLIWLLTVVALLPNFFVGSLEYDPRIYSCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 FYVEVIEATOWAPLNOIGLAVAINEGEMAEGIPEGLEVTSYTTAYENSOINATYYGLLNQ 313
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                                                                                                                                                                                                                                                                                                                                                                                                                 67 FNFKLENAGNIETVSLALADIVVAFYPYPITIVATFYDGWALGEEHCKASAFVMGLSVIG 126
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                                                                                                                                                                                                                                                                                                                                                        67 FEARMETETHIS ILNEAVAL-VESMULT FELAT, MAASEWEESEVELTHUVILLEGENGET 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AVRPGW------SGAGSARPSRTPRPPWVAPA--LSAVLIVTTAVDVVGNLLVILSVL 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 LALAYGAVII----LGVSGNLALIIIILKQKEMRNVINILIVNISESFILLVAIMCLPETE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ASTPSWNASSPRAASGRGENRTLVGRAFSAGARAVLVEVLYLLVCAAGIGGNTI VIYVVI 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%; Shore 337.5; DR 2; Longth 363;
29.3%; Pred. Mc. 1.2c.21;
ative 62; Mismatches 136; Indels 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed. No. 9e-22;
Mismatches 117; Indels
-VVVIVEAGGMLPEFTVNIVNLAVAL PQEP 280
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Aintron: #status absent

A:Intron: #status absent

C:Superfamily vertebrate rhodopsin

C:Superfamily vertebrate restatus predicted <TM2\
E:10-60-70-0main transmembrane #status predicted <TM2\
E:114-135/Domain transmembrane #status predicted <TM5\
E:124-6273/Domain transmembrane #status predicted <TM5\
E:224-6273/Domain transmembrane #status predicted <TM5\
E:230-0307/Comain transmembrane #status predicted <TM5\
E:230-0307/Comain transmembrane #status predicted <TM5\
E:132-0-137/Sinding site carbohydrate (Asn) (covalent) #status predicted

E:112-186/Disulfide bonds: #status predicted

E:112-186/Disulfide bonds: #status predicted

E:123-135/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by cAMP-depen
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A:Title: Cloning, functional expression and pharmacological characterization of a fourth A:Reference number: JN0762; MUID:93384611
A:Accession: JN0763
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A:Cross-references: GDB:138452: GM:M:192458
A:Map position: 16p13.3-16p13.3
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A:Residues: 1-364 <YAM>
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:Comment: This protein is a member of somatostatin receptor family.
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| Date | 30:Sop:1993 #sequence_rovision 20:Aug-1994 #text_chango 20:Tun-20:00
           291 A. H. SAGLYFEVVILSYANSGANFOLY STUSCINFFLSTUKVOLLLEL CLIFT STANFOLICE
                                                                                                          282 APQIPEGLEVTSYLLAYENSCLNAIVYGLLNQNEREEKRILLALWNPRHCIQDASKGSH 341
                                                                                                                                                                                                                               234 RVGCVPPPSEPKVTPMVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                              182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 Y-----DP-RIYSCTFIQTASTQYTAAVVVIHELLPIAVVSFCYLFIWVUVUQA-- 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVENITAIAINRYCYICHSMAYHRIYBBWHTF----LHICLIWLLTVVALLENFEVGSLE 182
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                                                                                                                                                                                                                                                                                                                        -----PRKAKPESPLCLKPSDLRSFITMFVVFVIFAICWAP---LNCIGLAVAINPQEM 281
                                                                                                                                                                                                                    ----VVVLVFAGCWLPFFTVNIVNLAVAL-PQEP 280
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that profit by Y throughton NEY-1 - mouse
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F:39-61/Fomain: transmembrane *status predicted <TW1>
E:73-93/Fomain: transmembrane *status predicted <TW2>
E:74-93/Fomain: transmembrane *status predicted <TM3>
E:114-135/Domain: transmembrane *status predicted <TM4>
E:113-231/Domain: transmembrane *status predicted <TM5>
E:261-85/Domain: transmembrane *status predicted <TM5>
E:262-85/Domain: transmembrane *status predicted <TM5>
E:262-125/Domain: transmembrane *status predicted <TM5>
E:262-125/Domain: transmembrane *status predicted <TM5>
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A:Besidues: 1-343, UDYETIAMSTHHITUSKTSLKGASPVAFKKISMNDNEKI - KPAN
A:Besidues: 1-343, UDYETIAMSTHHITUSKTSLKGASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKASPVAFKA
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FEBS Lett. 271, 81-84, 1990
A.Tit.b. Molecular cloning of a nevel G protein coupled receptor that may belong to the A.Feference number: S12863; MCID:91032093
A.Accession, S12863.
A.Accession, S12863.
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R:Krause, J.: Eva, C.: Seeburg, P.: Sprengel, P.

A:Description: Pharmacological and Transduction Properties of a Perombinantly
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A, Fesidues: 1:349 ~EVA>
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C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20 Apr-2000
C;Accession: S12863; S19101
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A:Cross-references: EMH::Z18280: NID:g53438; PIEN:CAA79157.1; PID:g53439
C:Superfamily: neurokinin l receptor
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C:Species Mus Musculus (Louse mouse)
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From. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
V.Title. Cloud luman neuropoptide Y receptor couples to two different second messender (Reference number: A46133; MUID:92335194

CACCOSSIONE 846133
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:Accession: $27388
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:Superfamily: neurokicis l :reoptor
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| Sporter: Mis muscuris (Douse mouse)
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Tate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                   :Molecule type: nucleic acid
:Residuce: 1-382 >HER>
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ett. 314, 186-188, 1991
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99 VAIFYDGWALGEEHCKASAFVMGLSVIGSVENITAIAINRYCYICHSMAYHRIYHEW--- 155
                                                       42 LALAYGAVII-----LGVSGNLALIIIILKQKEMBNVTNILIVNLSFSDLLVAVMGLPFTF 97
                                                                                                            RELEASE TAPALSAVLIVITAVDVVCNLLVILSVLENEKLENAGNLELVSLALAGLVVAFYFYFILL 98
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90; Conservative 55; Mismatches 11
                                                                                                                                                                                                      Sallia tatatata
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                                                                                                                                                                             Conservative
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                                                                                                                                                                                                      17.7%; Score 337, EB:
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C:Superfamily: vertebrate rhodopsin
E:47-73/Emmaln: transmembrane #status predicted <TM2>
E:41-79/Emmaln: transmembrane #status predicted <TM2>
E:104/Emmaln: transmembrane #status predicted <TM3>
E:104/Emmaln: transmembrane #status predicted <TM4>
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E:105-104/Emmaln: transmembrane #s
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A.Mag position: 20pll.2:20pll.2
A:Introps: #status absent
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A;Title: Cloning and characterization of a fourth human somatostatin recoptor
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A; Residues: 1-388 <YA
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                              MELATONIN KECEPIOK TYPE 10 (MEL-10-R) (ČKB).
Ballus dalius (Chicken).
Eukhyryota, Motaboa, Obordata, Crabiata, Vertebrata, Euteleostomi
                   Archosauria: Aves: Neognathae; Galliformes; Phasianidae; Phasianinae
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SEQUENCE FROM N.A. MEDLINE-9607355; PubMed-7576045;
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INTERPRO: IPPO02279; -
PEAM, PEDO001: 7tm_1:
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Pred. No. 9.2e-72;
5, Mismatches 67, Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright It is produced through a collaboration between the Swiss Institute of Richiformatics and the EMRI cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a livense agreement (Sar http://www.ist-sib ch/announce/
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GCRDB; GCR_0935; -
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Proc. Natl. Acad. Sci. U.S.A. 91:6133-6137(1994).
-!- FUNCTION: HIGH AFFINITY PROEPTOR POR MELATONIN, LIFETY TO MEDIATE
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INTERPRO: IPRO00276; -.
INTERPRO: IPRO02279; -.
PFAM: PF00001; 7tm_1; 1
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SUBSCRIPTIVE PROTEIN. INTEGRAL MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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01-FEB-1996 (Pel. 33, Last sequence update)
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WELATONIN RECEPTOR TYPE 1A (MEL-1A-F) (CKA).
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics (and the EMBL outstation the European Bioinformatics Institute. There are no instrictions on its
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Eukaryota, Metazoa, Chor
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Archosauria, Aves; Neoghathae, Galliformes, Phasianidav, Fhasianinae;
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                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN OPTIC TECTIM AND RETINA, LESS
NEOSTRIATUM, HYPOTHALAMUS AND THALAMUS.
SIMILARITY FELDINGS TO FAMILY 1 OF 3 EFFIELD CONTROL FUNCTIONS.
                                                                                                                                                                                                                FUNCTION: HIGH AMEINLIY RECEPTOR FOR MELATONIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE O PROTEINS THAT INHIBITS ADENVLATE CYCLASE ACTIVITY (BY SIMILARITY).
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Pred. No 1
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BY SIMILARITY.
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ng as its content is in no
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P49217:
11-PEH-1996
11-NOV 1997
15-JHL-1998
               "1-FEB-1996 (Rel. 33, Created)
1-NOV 1997 (Rel. 35, Last sequence update)
15-JUL 1998 (Ee) 36 [ast annotation update)
MELATIONIN RECEPTOR TYPE 1A (MEL-1A-R).
     MINRIA
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INTERPRO; IPR000276;
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CYTOPLASMIC (POTENT)
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N-LINKED (GLONAC
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PPEAM; PE000237; GPCPHPUOPSN.
PRINTS: PR00857; MELATONINR.
PPINTS: PP01149; MELATONINIAR.
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                                                                                                                                                                                                            DISULFID
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PROSITE: PS50252; S_FROTFIN_PECEP_F1_2; 1
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Neuron 13:1177-1185(1994).
-:- FUNCTION: HIGH APPINITY PROPERTY (** ***)
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Eukuryota: Metazoa: Chordata: Craniata: Vertebrata: Eutoloostomi:
Manmalia: Eutheria: Fodentia: Soluroynathi: Muridae: Crictinae:
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Submitted (NeV-1996) to
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TISSUE SPECIFICITY: AI LEAST IN THE BAND, MORE PRECISELY IN THE PARS THERALIS AND THE SUPPACHLASMALIC NUCLEUS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oning and characterization of a mammalian melatonin receptor that
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MKGNGSTILNASQQA-----PGVGEGGG-----PRPSWLASTLAFILIFTTVVDILGNL 49
                               MSENGS-FANCCEAGGWAVFPGWSGAGSAFFSFTFFFFWVAFALSAVLIVTTAVDVVGNL
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                                                                 Score 1112: DB 1: Pred No 9 56-70; C. Mismatidas T6.
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7 (POTENTIAL).

GYPCPLASMIC (PUTENTIAL).

BY SIMILARITY.

N-LINKED (SICNAC. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).

224ABBIDUSH SHACU CRC64;
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NIERBRAC IRRODOZEG:

PEAM: PEOGOO1: FUEL; 1.

PROSITE PSG0237 G_PROTEIN_PEOGEF_F1_1.

PROSITE: PSG0262: G_PROTEIN_PEOGEF_F1_2.

PROSITE: PSG0262: G_PROTEIN_PEOGEF_F1_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-001-1996 (Rel. 34, Created)
01-001-1996 (Rel. 34, Last sequence update)
01-001-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- FUNCTION: HIGH AFFINITY PECEPTOP FOR MELATIONIN THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PEPTUSSIS TOXIN SENSITIVE G PROTES THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
--- TISSUE SPECIFICITY: RRAIN AND KILNEY, WITH TRACE LEVELS IN LUNCESTMILLARITY; BELOWES TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu F., Yuan H., Sugamori K.S., Hamadanizadeh A., Lee F.2 S., Pang S.F., Brown G.M., Pristupa Z.B., Niznik H.B.; "Molecular and functional characterization of a partial cuNA encoding a novel chicken brain melatonin receptor."; FEBS Lett. 374:273-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELATONIN RECEPTOR TYPE IB (MEI-15-R) (FRAGMENT)
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                                                                                             NIVACO
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL)
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ML1A_HUMAN
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Best Local
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P48039;
          Okawa M., Takahashi K., Yamauchi T.;

"Allel: variants of human melatonin la receptor: function and prevalence it subjects with circarian rhythm sleep disorders.";

Biochem. Biophys. Res. Commun. 260:932-837(1949).

-i. FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES THE REPROPOUNTIVE AND CIPOADIAN ACTIONS OF MELATONIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PEPTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ACENVELATE OF THIS PROFILING WEDATION OF THIS SECOFICORY. EXPRESSED IN HYPOPHYSEAL PARS THREPALIS AND TISSUE SECOFICITY. EXPRESSED IN HYPOPHYSEAL PARS THREPALIS AND
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MELATONIN PECEPTOR TYPE 1A (MEL-1A-R).
                                                                                                                                                                                   Ebisawa T., Kajimura N., Uchiyama M., Katoh M., S
Watanabe T., Gueki Y., Ikeda M., Jodoj T., Sugisk
Kamel Y., Kim K., Shibul K., Kudo Y., Yamada N.,
                                                                                                                                                                                                                                                                                                          mediates reproductive and Neuron 13:1177-1185(1994).
                                                                                                                                                                                                                                       MEDLINE=99400459; PubMed=10471411;
                                                                                                                                                                                                                                                                           SECUENCE FROM N.A., AND VARIANTS IRP-54 AND VAL-157
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95033233; PubMed=7946354;
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                                                                                                                                                                                                                                                                                                                     pert S.M. Weaver D.P., Ebisawa T.:
coing and characterization of a mammalian melatonin receptor that
lates reproductive and circadian responses.";
HYPOTHALAMIC SUPRACHIASMATIC NUCLEI
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PRINTS: PRO0857: MELATONINE.
PRINTS: PRO0857: MELATONINE.
PRINTS: PRO0857: MELATONINIAR.
PROSITE: PRO0237: G_PROTEIN_PECEP_F1_1: 1
PROSITE: PRO0237: G_PROTEIN_PECEF_F1_2: 1
PROSITE: PRO0252: T_RESEMEMBRADE: Glycoprotein: Polymorphism.
PROSITE: PRO0252: T_RESEMEMBRADE: Glycoprotein: Polymorphism.
PROMETE: PRO0252: T_RESEMENDED: GLYCOPTENTIAL).

**TOTALIN: PRO0451: POLYMORPHISM.
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INTERPRO: IPPOOQ276: -.
INTERPRO: IPROO2278: -.
INTERPRO: IPRO02278: -.
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256 VEVIFAICWAPLNCIGLAVAINFWEMAPWIPEGLEVISYLLAYENSCLNAIVYGELNWNE
                                             183 VSSAYTIAVVVEHELVEMIIVIECYLEIWILVLQVEQEVKEDEKEKLKEQDEENEVIMEV 242
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                                                                                                                                                                                                                                                                                                                          4 GNGSALPNASOPVLEGDGARPSWLASALACVLIETIVVDILGNLLVILSVYRNKKLRNAG 62
                                                                       ASTOYTAAVVVIHEIIPIAVVSECYLPIWVLVLOABPKAKPESBLCIKPSDIBSELTMEV 255
                                                                                                                                                                                                                               NIFVVSLAVADLVVAIYPYPLVLMSIFNNGWNLGYLHCQVSGFLMGLSVIGSIFNITGIA 122
                                                                                                                                     INRYCYICHSIKYEKEYSSKNSLCYVELIWELTLAAVLENERAGTLQXEFFIYSGTFAGS 182
                                                                                                                                                                                  INRYCYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLPNEFVGSLEYDPRIYSCTEIQT 195
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AB029933; BAA85303.
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51.2%;
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Pred. No. 4.
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N-LINKED (GLONAC...) (POTENTIAL).
E -- W (ENTEX SIGNIE) (ANTLY REFORED H(MAX) AND SLIGHTLY ENHANCED AFFINITY).
(FTIG+VAR_009260.
A -- V (SIMILAR BINDING CHARACTERISTICS COMPARED TO WILD TYPE).
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: DF?db7lllDZ*&bEL GRC54;
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTCPLASMIC (
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RESULT 8
MILA_MOUSE
ID MILA_MOUSE
AC Q61184;
DT 01-NQV-1997;
                                       U14TÜSTU
NIVWOG
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Endaminiology 137:3469-3477(996).
-:- EUNCLICH: HIGH AFFINITY PECEPTOR FOR MELATONIN. LIKELY TO MEDIATES
-:- EUNCLICH: HIGH AFFINITY PECEPTOR OF MELATONIN. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY PRETUSSIS TOXIN SENSITIVE G
PROTEINS THAT INHIBITS ADENVIATE OFCHASE ACTIVITY (BY SIMILARITY).
-!- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBCELULAR LOCATION: TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0857; MELATONINR. PRINTS; PRO1149; MELATONIN1AR PROSITE; PSO0237; G_PROTEIN_RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed usage by and four-times requires a librage agreement (whe http://www.ishrs.icor.send.an email to license@isb-sib.ch).
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01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
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Mammalia: Eutheria: Rudentia: Shiurognathi: Muridae, Murinae: Mus
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                                                                                                                                                                                                                                                                                                                                G_PROTEIN_RECEP_F1_1; 1.

G_PROTEIN_RECEP_F1_2; 1.

G_PROTEIN_RECEP_F1_2; 1.

1. **COPTON** TRANSMORDER** S1ycoprotein.
32 EXTRACELULAR (POTENTIAL).

S3 1 (POTENTIAL).
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35, Last sequence update)
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N-LINKED (GLONAC:
                                       CYTOPLASMIC (POTENTIAL).
BY SIMILARITY
                                                                                 EXTRACELLULAR (POTENTIAL) 7 (POTENTIAL).
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6 (POTENTIA)
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Best Local
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Mel la melatonin receptor.":

Bicchim Biophys Acta 1350 (2020-107) 1997

Bicchim Biophys Acta 1350 (2020-107) 1997

THE REPRODUCTIVE AND CIFCADIAN ACTIONS OF MELATONIN THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY

--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED MECHANISMS.

--- SIMILARITY: RELONGS TO FAMILY 1 OF 3-PROTEIN COUPLED MECHANISMS.
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                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PITUITARY PARS TUBERALIS:
MEDILINE-9503233: FubMed-7046354:
Reppert S M, Wear D P, Ebisawa T.;
Reppert S M of a mammalian melatonin receptor that
mediates reproductive and circadian responses.";
Neuron 13:1177-1185(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P48040: 045508:

01-FER-1946 (Rel 33, Created)

01-FEB-1996 (Rel 31, last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITA_SHEEP
                                                                                                                                                                                                                                                                                                      Barrett P., Conway S., Joskers P., S
Guardiola-Lemaitre B., Delagrange P.
                                                                                                                                                                                                                                                                                                                         MEDLINE=97337902; PubMed=9194573; Barrett F. Conway S., Indkers F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N A.
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PRINTS: PRO01149: MELATIONINIAR.

PROSITE: PS00237: G_PROTEIN_PECEP_F1_2: 1.

PROSITE: PS50252: G_PROTEIN_PECEP_F1_2: 1.
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                                                                     302 CLNAIVYSLLNÓNFFFEYKRILLALWNPRHOTODASKGSH-AEGLÓSFAFPII
                                                                                             245 TKPUDEFNEVIMEVVEVLEAICWAPENFIGUVVASDPASMAPRIPEWLEVÄSYYMAYENS
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BY SIMILARITY
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N-LINKED (GLONAC )) (POT
A -- 2 (IN MEL 1A(BETA))
H -> 8 (IN MEL 1A(BETA))
1 -> V (IN MEL 1A(BETA))
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Pred. No. 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae, Homo.
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0) NOV-1997 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                             NIAMOG
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INTERPRO: IPROGO2280:
PFAM; PFOUGG1; /tm_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reppert S.M., Weaver D.R., Ebisawa I., Mahle C.D.
Kolakowski L.F. Jr.;
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                                                                                                                                                                                                                                          TRANSMEM
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  148
                                                                                                                                       Local similarity
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, σCP_1930; -,
, 30000; -,
YHRIYRRWHIPLHICLIWLLTVVALLPNFFVGSLEYDPRIYSCIFIQIASIQYIAAVVVI
                       LVAIYFYFLMLHAMSIGGWDLSQLQCQMVGFITGLSVVGSIFNIVAIAINFYCYICHSLQ 135
                                                                           KIPOPEY-PPALITEMETAMVITIVVHLIGNSMVILAVIKNKKLENSGNIEVVSLSVAHM-75
                                                                                                RTPRPPWVAPAL----SAVLIVTTAVDVVGNLLVILSVLENEKLENAGNLFIVSLALADI 87
                                                VVAFYPYPLILVAIFYDGWALGEEHCKASAFVMGLSVIGSVFNITAIAINPYCYICHSMA 147
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35, Last sequence update)
39, Last annotation update)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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Q28558: Q46624;
Q1-NOV-1997 (Pe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reppert S.M., Weaver D.R., Ebisawa T., Mahle C.D.,
Kolakowski L.F. Jr.;
"Cloning of a melatonin-related receptor from human pituitary.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exemple: Fariett F. Williams E.M. Commay S. Mordan P.J.: "The evine melatenin-related receptor: cloning and preliminary distribution and binding studies.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Pukaryota Mefazoa: Chordata Craniata: Vertebrata: Euteleostomi:
Mammalia: Pubbria Tetarticdautyla: Euripantia: Per ru Bur 19-a
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15-JUL-1999 (Rel. 38, Last annotation update)
MELATUNIN-RELATED RECEPTOR (H9).
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                                                                                                                                          DOMAIN
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PROSITE: PS00237: G_PROTEIN_RECEP_F1_1: 1.

PS08ITE: FS50050: G_PROTEIN_RECEP_E1_0: 1.
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  TRANSMEM
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INTERPRO: IPRO02280;
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-!- FUNCTION: DOES NOT BIND MELATONIN (BY SIMILARITY).
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15-DEC-1998 (Rel
15-JUL-1999 (Rel
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                                                                                                             CRANSMEM
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  STANDARD;
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1 (POTENTIAL).
CYTOPLASMIC (POTENT)
4 (POTENTIAL).
FXIRACELLULAR
5 (POTENTIAL).
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CYTOPLASMIC (
                                                                                                                                       2 (POTENTIAL)
EXTRACELLULAR
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Best Local S
Matches 150
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TRANSMEM
DOMAIN
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                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as as its content is in moderated and this statement is not removed. Usage by and for commencentities requires a license agreement (see http://www.sbisib.ch/annousor send an email to license@ish-sib.ch).
                                                                                                                                                                                "Assignment of the melatonin-related receptor (GPR50) and mouse chromosome X (Gpr50)."; Genomic 55.248-251(1999).
                                                                                                                                                                                                                                                                                                                                                                     15-DEC 1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
MELATONIN-RELATED RECEPTOR (H9).
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DOMAIN
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-99134305; PubMed=9933574;
                                                                                                                                                                                                                                                                                                                                                           GPR50
EMBL: AF065145: AAC21462.1: ALT_INIT
                                                                                                                                                   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae: Murinae; Mus
                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                              Bukaryota
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BY SIMILAPITY

P -> 1, (IN PEF 2)

I -> M (IN PEF 2)

ASD -> 7 (IN PEF 2)
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EXTENDELLULAR (POTENTIAL)

7 (POTENTIAL)
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6 (FOTENTIAL
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CYTOPLASMIC (
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2.5e-51;
tches 72; Indels
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Best Local Similarity
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-0.2763;
-15-JUL-1998 (Pel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Pel. 35, Last annotation update)
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PPINTS: PROINTS: PRONORS: G_PROTEIN_PROEP_F1_1: 1.
PROSTITE: PSC00237: G_PROTEIN_PROEF_F1_2: 1.
PROSTITE: PSC00262: G_PROTEIN_PROEF_F1_2: 1.
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INTERPRO: IPPO00276;
INTERPO: IPPO02280;
INTERPO: TPPO017778m.]
SEQUENCE FROM N.A.
TISSUE-HYPOTHALAMUS, AND PITUITARY;
MEDITUE-97262109; PubMed-9107687;
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DOMAIN
                                                                                                                             Eukaryota; Metazoa; Chordata; Crania:
Mammalia, Eutheria, Cetarticdactyla,
                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                          MINELA
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                                                                                                       Bovinae,
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47.8%; Fred. No. 9.6e-51;
Live 77; Mismatches 72;
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BY SIMILARITY.
DOI:35000485AL41: URU54;
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CYTOPLASMIC (
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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIVWOOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM: PF00001: 7tm_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Sage by and for commercial ontries requires a license agreement (See http://www.isb-eib-ch/announce.or send an email to license@isb-sib.ch).
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   ML1H_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothschild M.F.;
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THE REPRODUCTIVE AND CIRCADIA ACTIONS OF MELATONIN. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY PERFUSSIS DOIN SENSITIVE G
PROTEINS THAT INHIHITS ADENYLATE GYCLASE ACTIVITY.
                                                                                                                                                                    181
                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                              154 RWHTPLHICHIWHITVVALLPNEFVGSLEYDPRIYSCTEIQTASTQYTAAVVVIHELLPI 213
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                                                                                                                                                                                                                                                                                                                                                                                                                     94 YPUILVAIFYDGWALGEEHCKASAFVMGLSVIGSVENITAIAINRYCYICHSMAYHRIYR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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SIMILABITY: RELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                               VDSSNHVAHRIKEKESE NOT
                                                                                                                               ODASKOSHAFGI OSPAP 359
                                                                                                                                                                                                                                       LVVIFCYLRIWALVLOVEWRVKPDNKPKLKPODFPNFVTMFVVFVLFAICWAPLNFIGLV 180
                                                                                                                                                                                                                                                                           AVVSECYLPIWVLVLQARPKAKPESFLCLKPSOLFSELTMEVVEVIFAICWAPLNCIGLA 273
                                                                                                                                                                                                                                                                                                              STNSLCYVELIMMLTLVAIVPNLCVGTLQYDPRIYSCTFTQSVSSAYTIAVVVEHFIVPM 120
                                                                                                                                                                                                                                                                                                                                                                                 YPLALAS INNOVESTI SEGESSIFLMSESVISSVENITGIAINPYDSICHSESYNKEYS 50
                                                                                                                                                                    VASEPASMAPPIPEWLEVASYYMGYENSCLNAIIYGLLNQNEPQEYPKIIVSLCTTKMEF 240
                                                                                                                                                                                                    VAINPQEMAPQIPEGLEVTSYLLAYENSCLNAIVYGLINQNEPPEYKRIIIALWNPRHCI 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.88;
59.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Mismatches 51, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 835; DB 1;
Pred. No. 7.1e 51;
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CYTOPLASMIC (
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EXTRACELLULAR (POTENTIAL)
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RESHLT 15
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Bost Local :
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n1-org1-946 (Pel 34, Greated)
01-org1-1946 (Rei 34, Last sequence update)
61-org1-1946 (Fel 34, Last sequence update)
61-org1-1946 (Fel 34, Last sequence update)
MELATIONIN RECEPTOR TYPE 18 X1.7 (MEL-18-R) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and frontities requires a lovense agreement (see http://www.isb.sib.or.seed an email to liceuse@isb.sib.ch).
MINI_BRARE STANDARD: P51049
01-021-1996 (Rel. 34, Created)
01-021-1996 (Pr) 34, Tast sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTIE: PSO0227; G_PROTEIN_PECEP_F1_1: PARTIAL.
PROSTIE: PSS0262: G_PROTEIN_PECEP_F1_2: 1.
G-protein coupled receptor. Transmembrane. Glycoprotein
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-:- FUNCTION: HIGH AFFINITY PECEPIGE FOR MELATIONIN. THE ACTIVITY OF THIS FUNCTION: HIGH AFFINITY PERFUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Amphibia: Hatrachia; Anura; Mesobatrachia, Fipoidea, Pipidae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor subtypes differentially expressed in chick brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kolakowski L.F. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reppert S.M.,
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                                                                                                                                                                                                 264 WAPLNCIGLAVAINPQEMAPQIPEGLEVTSY 294
                                                                                                                                                                                                                                                                                 204 VVVIHELLPIAVVSECYLEIWVLVLQAREKAKPESRIGLKPSDLRSFLIMEVVEVIFAIC 263
                                                                                                                                                                                                                                                                                                                                                               144 HSMAYHRIYRRWHTPLHICLIWLLTVVALLPNEFVGSLEYDPRIYSCTEIQTASTQYTAA 203
                                                                                                                                                                                                                                       61 VVVIHFILPITVVTFCYLRIWILVIQVERKVKSEFKPRMKQSDERNFLTMEVVEVIFAFO
                                                                                                                                                                                                                                                                                                                                                                                      Ja.
Domai
106;
                                                                                                                                                                WAPLNFIGLAVSINPTEVAPKIPEWLFVVSY
                                                                                                                                                                                                                                                                                                                       HSEVYEKLESLWNTILYVCLIWTITVVATVPNEFVGSLEYDPRIYSCTEVQTVSSSYTIT 60
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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30 68
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                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 584; DB 1;
Frad No. 7.3e-34;
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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                                                               PRT;
                                                               153 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 152;
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Best Local Similarity
Matches 107; Conserv
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SEQUENCE
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PROSITE: PS00237: G_PROTEIN_RECEP_F1_1: PARTIAL.

PROSITE: PS00262: G_FROTEIN_RECEF_F1_2: 1.
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Neuron 15:1003-1015(1995).

-!- EUNCTION- HIGH AFFINITY PRCEPTOR FOR MELATONIN. THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS
THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

-!- SUBCELLULAR LOCATION- INTEGRAL MEMBRANE PROTEIN.

-!- SIMILARITY- HELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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ZFIN; ZDB-GENE-990415-156; MEL1BR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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STIC-Biotech/ChemLib

Pak, Michael Friday, February 02, 2001 2:17 PM STIC-Biotech/ChemLib

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From: Sent: To: Subject:

sequence search 09/226,046

Sequence search - 2 month amendment due by 2/24/01 App. #: 09/226,046
Result format: Paper.

Title: High affinity melatonin receptors and uses thereof

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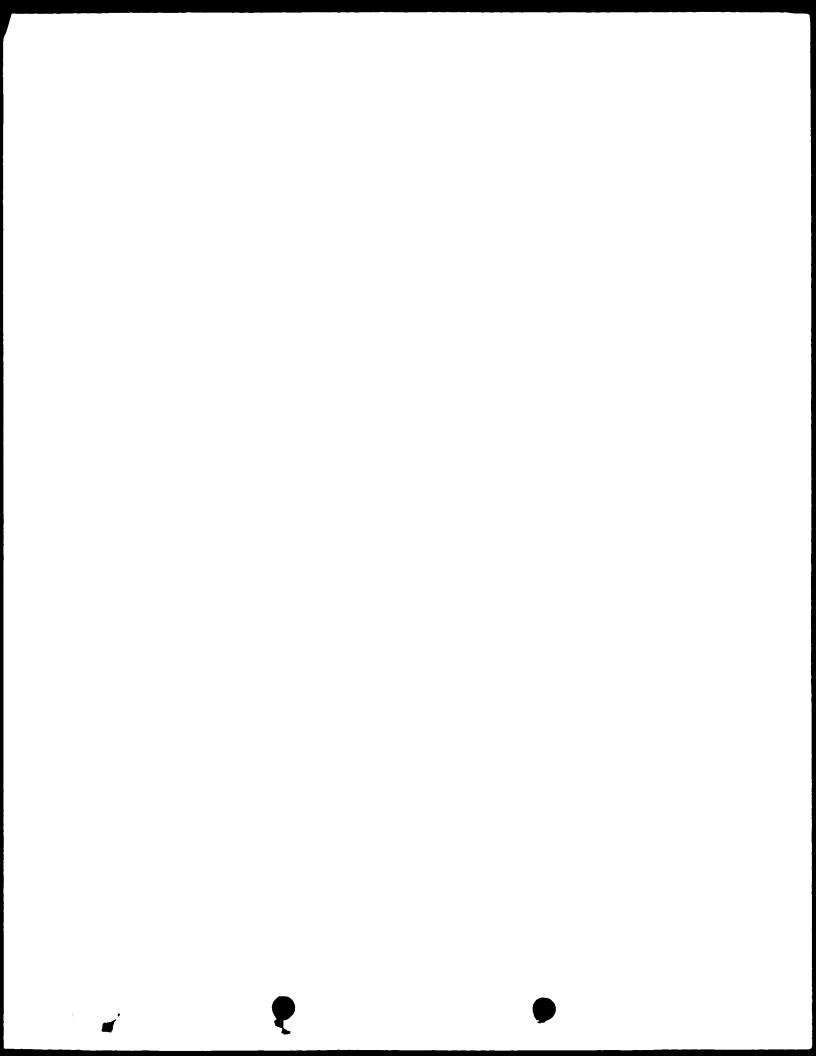
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1) SEQ ID NO: 5, 6, 11, 12, 15, and 16. Reverse translate NO:12

Thanks,

Mike Pak

Michael D. Pak 305-7038 CM-1; Rm. 10E13 AU 1646 - USPTO



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Journal code: HIV. ISSN: 0021-9258.

JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Jan 15) 266 (2) 1354. OS

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               Department of Medicine, Beth Israel Hospital, Boston,
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         tissues [published erratum appears in J Biol Chem 1991 Jan
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Cloning and expression of the human substance

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Center-Wadsworth, Los Angeles, CA 90073.

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